1

4



SEQUENCE LISTING

- <110> Yen, Frances
 Erickson, Mary Ruth
 Fruebis, Joachim
 Bihain, Bernard
- <120> Methods Of Screening For Compounds That Modulate the LSR-Leptin Interaction and Their Use in the Prevention and Treatment of Obesity-Related Diseases
- <130> 70.US2.REG
- <150> 60/155,506
- <151> 1999-09-22
- <160> 106
- <170> Patent.pm
- <210> 1
- <211> 23187
- <212> DNA
- <213> Homo sapiens
- <220>
- <221> exon
- <222> 2001..2356
- <223> exon1.
- <220>
- <221> exon
- <222> 3540..3884
- <223> exon2
- <220>
- <221> exon
- <222> 12163..12282
- <223> exon3
- <220>
- <221> exon
- <222> 15144..15200
- <223> exon4
- <220>
- <221> exon
- <222> 15765..15911
- <223> exon5
- <220>
- <221> exon
- <222> 19579..19752
- <223> exon6
- <220>
- <221> exon
- <222> 19899..19958
- <223> exon7
- <220>

```
<221> exon
<222> 20056..20187
<223> exon8
<220>
<221> exon
<222> 20329..20957
<223> exon9
<220>
<221> exon
<222> 21047..21187
<223> exon10
<220>
<221> polyA signal
<222> 21168..21173
<223> AATAAA
<220>
<221> misc_feature
<222> 1..2000
<223> potential 5'regulatory region
<220>
<221> misc_feature
<222> 22324..23187
<223> homology with USF2 gene in ref: embl Y07661
<220>
<221> primer bind
<222> 523..544
<223> upstream amplification primer 17-2
<220>
<221> primer_bind
<222> 1047..1068
<223> downstream amplification primer 17-2 , complement
<220>
<221> primer_bind
 <222> 946..963
 <223> upstream amplification primer 99-4576
 <220>
 <221> primer_bind
 <222> 1385..1402
 <223> downstream amplification primer 99-4576 , complement
 <220>
 <221> primer bind
 <222> 1096..1115
 <223> upstream amplification primer 9-19
 <220>
 <221> primer_bind
 <222> 1616..1635
 <223> downstream amplification primer 9-19 , complement
 <220>
 <221> primer_bind
 <222> 1602..1621
 <223> upstream amplification primer 9-20
```

```
<220>
<221> primer bind
<222> 2074..2093
<223> downstream amplification primer 9-20 , complement
<220>
<221> primer_bind
<222> 2036..2053
<223> upstream amplification primer 99-4557
<220>
<221> primer bind
<222> 2563..2580
<223> downstream amplification primer 99-4557 , complement
<220>
<221> primer_bind
<222> 2084..2102
<223> upstream amplification primer 9-1
<220>
<221> primer_bind
<222> 2483..2500
<223> downstream amplification primer 9-1 , complement
<220>
<221> primer bind
<222> 2470..2489
<223> upstream amplification primer 9-21 , complement
<220>
<221> primer_bind
<222> 2062..2081
<223> downstream amplification primer 9-21
<220>
<221> primer bind
<222> 3455..3474
<223> upstream amplification primer 9-3
<220>
<221> primer_bind
<222> 3882..3901
<223> downstream amplification primer 9-3 , complement
<220>
<221> primer bind
<222> 3775..3792
<223> upstream amplification primer 99-4558
<220>
<221> primer_bind
<222> 4336..4356
<223> downstream amplification primer 99-4558 , complement
<220>
<221> primer_bind
<222> 4902..4920
<223> upstream amplification primer 99-14419 , complement
<220>
<221> primer_bind
```

```
<222> 4444..4463
<223> downstream amplification primer 99-14419
<221> primer bind
<222> 6638..6655
<223> upstream amplification primer 99-4577
<220>
<221> primer_bind
<222> 7072..7089
<223> downstream amplification primer 99-4577 , complement
<220>
<221> primer bind
<222> 7995..8012
<223> upstream amplification primer 99-4559
<220>
<221> primer_bind
<222> 8576..8593
<223> downstream amplification primer 99-4559 , complement
<220>
<221> primer_bind
<222> 9622..9639
<223> upstream amplification primer 99-3148
<220>
<221> primer_bind
<222> 10023..10040
<223> downstream amplification primer 99-3148 , complement
<220>
<221> primer_bind
<222> 9964..9981
<223> upstream amplification primer 99-4560
<220>
<221> primer bind
<222> 10546..10563
<223> downstream amplification primer 99-4560 , complement
<220>
<221> primer_bind
<222> 10996..11015
<223> upstream amplification primer 99-14411 , complement
<220>
<221> primer bind
 <222> 10492..10512
 <223> downstream amplification primer 99-14411
 <220>
 <221> primer_bind
 <222> 11972..11990
 <223> upstream amplification primer 99-4561
 <220>
 <221> primer_bind
 <222> 12481..12501
 <223> downstream amplification primer 99-4561 , complement
```

```
<220>
<221> primer bind
<222> 12005..12023
<223> upstream amplification primer 9-4
<220>
<221> primer_bind
<222> 12417..12436
<223> downstream amplification primer 9-4 , complement
<220>
<221> primer_bind
<222> 14102..14119
<223> upstream amplification primer 99-4562
<220>
<221> primer_bind
<222> 14543..14563
<223> downstream amplification primer 99-4562 , complement
<220>
<221> primer_bind
<222> 14431..14448
<223> upstream amplification primer 99-3149
<220>
<221> primer_bind
<222> 14848..14865
<223> downstream amplification primer 99-3149 , complement
<220>
<221> primer bind
<222> 14748..14767
<223> upstream amplification primer 9-22
<220>
<221> primer_bind
<222> 15198..15218
<223> downstream amplification primer 9-22 , complement
<220>
<221> primer bind
<222> 14748..14767
<223> upstream amplification primer 9-24
<220>
<221> primer bind
<222> 15333..15351
<223> downstream amplification primer 9-24 , complement
<220>
<221> primer bind
 <222> 15002..15019
 <223> upstream amplification primer 9-5
 <220>
 <221> primer_bind
 <222> 15333..15351
 <223> downstream amplification primer 9-5 , complement
 <220>
 <221> primer_bind
 <222> 15640..15657
```

```
<223> upstream amplification primer 9-6
<220>
<221> primer_bind
<222> 16072..16089
<223> downstream amplification primer 9-6 , complement
<220>
<221> primer_bind
<222> 15800..15817
<223> upstream amplification primer 99-4563
<220>
<221> primer bind
<222> 16179..16199
<223> downstream amplification primer 99-4563 , complement
<220>
<221> primer_bind
<222> 19295..19312
<223> upstream amplification primer 99-3150
<220>
<221> primer_bind
<222> 19729..19746
<223> downstream amplification primer 99-3150 , complement
<220>
<221> primer_bind
<222> 19420..19438
<223> upstream amplification primer 9-7
<220>
<221> primer_bind
<222> 19824..19841
<223> downstream amplification primer 9-7 , complement
<220>
<221> primer_bind
<222> 19798..19815
<223> upstream amplification primer 9-8
<220>
<221> primer_bind
 <222> 20137..20155
 <223> downstream amplification primer 9-8 , complement
 <220>
 <221> primer_bind
 <222> 19913..19931
 <223> upstream amplification primer 9-9
 <220>
 <221> primer_bind
 <222> 20329..20346
 <223> downstream amplification primer 9-9 , complement
 <220>
 <221> primer_bind
 <222> 20139..20157
 <223> upstream amplification primer 99-4564
 <220>
```

```
<221> primer_bind
<222> 20582..20599
<223> downstream amplification primer 99-4564 , complement
<220>
<221> primer bind
<222> 20238..20256
<223> upstream amplification primer 9-10
<220>
<221> primer bind
<222> 20645..20662
<223> downstream amplification primer 9-10 , complement
<220>
<221> primer_bind
<222> 20410..20424
<223> upstream amplification primer 9-26
<220>
<221> primer_bind
<222> 20690..20706
<223> downstream amplification primer 9-26 , complement
<220>
<221> primer_bind
<222> 20569..20588
<223> upstream amplification primer 9-23
<220>
<221> primer_bind
<222> 21243..21262
<223> downstream amplification primer 9-23 , complement
<220>
<221> primer bind
<222> 20583..20604
<223> upstream amplification primer 9-11
<220>
<221> primer_bind
<222> 21015..21034
<223> downstream amplification primer 9-11 , complement
<220>
<221> primer_bind
<222> 20584..20601
<223> upstream amplification primer 99-15285 , complement
<220>
<221> primer bind
<222> 20139..20158
<223> downstream amplification primer 99-15285
<220>
<221> primer_bind
<222> 20642..20659
<223> upstream amplification primer 99-15287 , complement
<220>
 <221> primer_bind
<222> 20207..20227
 <223> downstream amplification primer 99-15287
```

```
<220>
<221> primer bind
<222> 20691..20709
<223> upstream amplification primer 99-15286 , complement
<220>
<221> primer_bind
<222> 20238..20257
<223> downstream amplification primer 99-15286
<220>
<221> primer_bind
<222> 20943..20960
<223> upstream amplification primer 9-2
<220>
<221> primer_bind
<222> 21295..21312
<223> downstream amplification primer 9-2 , complement
<220>
<221> primer_bind
<222> 21013..21031
<223> upstream amplification primer 99-15284 , complement
<220>
<221> primer_bind
<222> 20582..20602
<223> downstream amplification primer 99-15284
<220>
<221> primer bind
<222> 21019..21038
<223> upstream amplification primer 99-14407 , complement
<220>
<221> primer_bind
<222> 20571..20589
<223> downstream amplification primer 99-14407
<220>
<221> primer_bind
<222> 21079..21097
<223> upstream amplification primer 99-15283 , complement
<220>
<221> primer_bind
<222> 20638..20655
<223> downstream amplification primer 99-15283
<220>
<221> primer bind
<222> 21013..21032
<223> upstream amplification primer LSRi9f15s
<220>
<221> primer_bind
<222> 21195..21214
<223> downstream amplification primer LSRi10r14s , complement
<220>
<221> primer_bind
```

```
<222> 20354..20372
 <223> upstream amplification primer LSRx9f13s
 <221> primer bind
 <222> 20570..20591
 <223> upstream amplification primer LSRx9f14s
 <220>
 <221> primer_bind
 <222> 20811..20832
 <223> downstream amplification primer LSRx9r13s , complement
 <220>
 <221> allele
 <222> 818
 <223> 17-2-297 : polymorphic base G or C
 <220>
 <221> allele
 <222> 1243
 <223>9-19-148 : polymorphic base C or T
 <220>
 <221> allele
 <222> 1374
 <223>9-19-256 : polymorphic base A or G
 <220>
 <221> allele
 <222> 1401
 <223>9-19-307 : polymorphic base A or T
 <220>
 <221> allele
 <222> 1535
 <223> 9-19-442 : polymorphic base deletion of C
 <220>
 <221> allele
 <222> 1788
  <223> 9-20-187 : polymorphic base A or C
 <220>
 <221> allele
  <222> 2391
  <223>9-1-308 : polymorphic base G or C
  <220>
  <221> allele
  <222> 3778
  <223>9-3-324 : polymorphic base C or T
  <220>
  <221> allele
<222> 4498
  <223> 99-14419-424 : polymorphic base T or G
  <220>
  <221> allele
  <222> 15007
  <223> 9-24-260 : polymorphic base A or G
```

```
<220>
<221> allele
<222> 15233
<223> 9-24-486 : polymorphic base A or G
<220>
<221> allele
<222> 15826
<223>9-6-187 : polymorphic base C or T
<220>
<221> allele
<222> 19567
<223> 9-7-148 : polymorphic base A or G
<220>
<221> allele
<222> 19744
<223> 9-7-325 : polymorphic base A or G
<220>
<221> allele
<222> 19786
<223> 9-7-367 : polymorphic base A or C
<220>
<221> allele
<222> 20158
<223> 9-9-246 : polymorphic base G or C
<220>
<221> allele
<222> 20595
<223> LSRX9-BM (17-1-240) : polymorphic base deletion of AGG
<220>
<221> allele
<222> 21108
<223> LSRX10-BM : polymorphic base T or G
<220>
<221> allele
<222> 606
<223> potential polymorphic base C or T
<220>
<221> allele
<222> 5141
<223> potential polymorphic base insertion of G
<220>
<221> allele
<222> 7428
<223> potential polymorphic base insertion of C
<220>
<221> allele.
<222> 8394
<223> potential polymorphic base C or G
<220>
<221> allele
<222> 8704
```

```
<223> potential polymorphic base T or C
<220>
<221> allele
<222> 9028
<223> potential polymorphic base G or A
<220>
<221> allele
<222> 9950
<223> potential polymorphic base deletion of GAATGAAA
<220>
<221> allele
<222> 9977
<223> potential polymorphic base T or C
<220>
<221> allele
<222> 10021
<223> potential polymorphic base A or G
<220>
<221> allele
<222> 11878
<223> potential polymorphic base C or T
<220>
<221> allele
<222> 19040
<223> potential polymorphic base deletion of G
<220>
<221> allele
<222> 21363
<223> potential polymorphic base A or G
<220>
<221> allele
<222> 21449
<223> potential polymorphic base C or T
<220>
<221> allele
<222> 21451
<223> potential polymorphic base G or C
<220>
<221> allele
<222> 21454
<223> potential polymorphic base A or G
<220>
<221> allele
<222> 21455
<223> potential polymorphic base G or A
<220>
<221> allele
<222> 21569
<223> potential polymorphic base T or A
<220>
```

```
<221> allele
<222> 21683
<223> potential polymorphic base deletion of C
<220>
<221> allele
<222> 21694
<223> potential polymorphic base insertion of T
<220>
<221> allele
<222> 21728
<223> potential polymorphic base deletion of G
<220>
<221> misc_binding
<222> 799..817
<223> 17-2-297.mis1
<220>
<221> misc_binding
<222> 819..837
<223> complement 17-2-297.mis2
<220>
<221> misc_binding
<222> 1224..1242
<223> 9-19-148.mis1
<220>
<221> misc binding
<222> 1244..1262
<223> complement 9-19-148.mis2
<220>
<221> misc binding
<222> 1330..1373
<223> 9-19-256.mis1
<220>
<221> misc_binding
<222> 1375..1393
<223> complement 9-19-256.mis2
<220>
<221> misc_binding
<222> 1382..1400
<223> 9-19-307.mis1
<220>
<221> misc_binding
<222> 1402..1420
<223> complement 9-19-307.mis2
<220>
<221> misc_binding
<222> 1516..1534
<223> 9-19-442.mis1
<220>
<221> misc_binding
<222> 1769..1787
<223> 9-20-187.mis1
```

```
<220>
<221> misc_binding
<222> 1789..1807
<223> complement 9-20-187.mis2
<220>
<221> misc_binding
<222> 2372..2390
<223> 9-1-308.mis1
<220>
<221> misc_binding
<222> 2392..2410
<223> complement 9-1-308.mis2
<220>
<221> misc_binding
<222> 3759..3777
<223> 9-3-324.mis1
<220>
<221> misc_binding
<222> 3779..3797
<223> complement 9-3-324.mis2
<220>
<221> misc_binding
<222> 4979..4997
<223> 99-14419-424.mis2
<220>
<221> misc binding
<222> 4999..5017
<223> complement 99-14419-424.mis1
<220>
<221> misc_binding
<222> 14988..15006
<223> 9-24-260.mis1
<220>
<221> misc_binding
<222> 15008..15026
<223> complement 9-24-260.mis2
<220>
<221> misc_binding
<222> 15214..15232
<223> 9-24-486.misl
<220>
<221> misc binding
<222> 15234..15252
<223> complement 9-24-486.mis2
<220>
<221> misc_binding
<222> 15807..15825
<223> 9-6-187.mis1
<220>
```

<221> misc_binding

```
<222> 15827..15845
<223 > complement 9-6-187.mis2
<220>
<221> misc binding
<222> 19548..19566
<223> 9-7-148.mis1
<220>
<221> misc_binding
<222> 19568..19586
<223> complement 9-7-148.mis2
<220>
<221> misc binding
<222> 19725..19743
<223> 9-7-325.mis1
<220>
<221> misc_binding
<222> 19745..19763
<223> complement 9-7-325.mis2
<220>
<221> misc_binding
<222> 19767..19785
<223> 9-7-367.mis1
<220>
<221> misc binding
<222> 19787..19805
<223> complement 9-7-367.mis2
<220>
<221> misc binding
<222> 20139..20157
<223> 9-9-246.mis1
<220>
<221> misc_binding
<222> 20159..20177
<223> complement 9-9-246.mis2
<220>
<221> misc_binding
<222> 20576..20594
<223> LSRX9-BM.mis1(17-1-240)
<220>
<221> misc_binding
<222> 20596..20614
<223> complement LSRX9-BM.mis2(17-1-240)
<220>
<221> misc_binding
<222> 21089..21107
<223> LSRX10-BM.mis1
<220>
<221> misc_binding
<222> 21109..21127
<223> complement LSRX10-BM.mis2
```

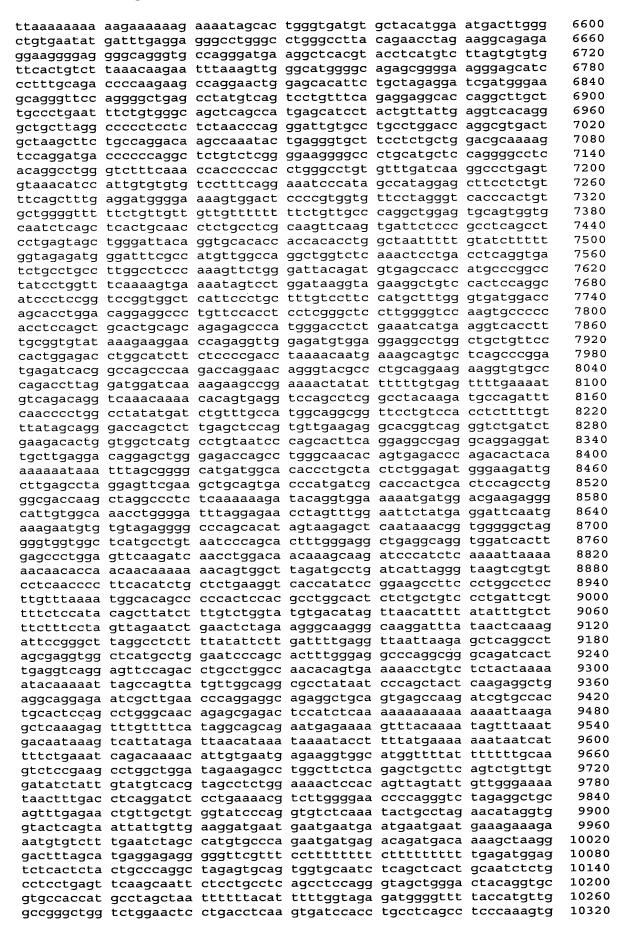
```
<220>
<221> misc binding
<222> 587..605
<223> potentialsite606.mis1 potential
<220>
<221> misc_binding
<222> 607..625
<223> complement potentialsite606.mis2 potential
<220>
<221> misc binding
<222> 5122..5140
<223> potentialsite5141.mis1 potential
<220>
<221> misc_binding
<222> 5142..5160
<223> complement potentialsite5141.mis2 potential
<220>
<221> misc_binding
<222> 7409..7427
<223> potentialsite7428.mis1 potential
<220>
<221> misc binding
<222> 7429..7447
<223> complement potentialsite7428.mis2 potential
<220>
<221> misc binding
<222> 8375..8393
<223> potentialsite8394.misl potential
<220>
<221> misc binding
<222> 8395..8413
<223> complement potentialsite8394.mis2 potential
<220>
<221> misc_binding
<222> 8685..8703
<223> potentialsite8704.mis1 potential
<220>
<221> misc_binding
<222> 8705..8723
<223> complement potentialsite8704.mis2 potential
<220>
<221> misc binding
<222> 9009..9027
<223> potentialsite9028.mis1 potential
<220>
<221> misc_binding
<222> 9029..9047
<223> complement potentialsite9028.mis2 potential
<220>
<221> misc_binding
<222> 9931..9949
```

```
<223> potentialsite9950.mis1 potential
<220>
<221> misc binding
<222> 9951..9969
<223> complement potentialsite9950.mis2 potential
<220>
<221> misc binding
<222> 9958..9976
<223> potentialsite9977.mis1 potential
<220>
<221> misc binding
<222> 9978..9996
<223> complement potentialsite9977.mis2 potential
<221> misc_binding
<222> 10002..10020
<223> potentialsite10021.mis1 potential
<220>
<221> misc_binding
<222> 10022..10040
<223> complement potentialsite10021.mis2 potential
<220>
<221> misc binding
<222> 11859..11877
<223> potentialsite11878.mis1 potential
<220>
<221> misc binding
<222> 11879..11897
<223> complement potentialsite11878.mis2 potential
<220>
<221> misc binding
<222> 19021..19039
<223> potentialsite19040.mis1 potential
<220>
<221> misc_binding
<222> 19041..19059
<223> complement potentialsite19040.mis2 potential
<220>
<221> misc binding
<222> 21344..21362
<223> potentialsite21363.mis1 potential
<221> misc_binding
<222> 21364..21382
<223> complement potentialsite21363.mis2 potential
<220>
<221> misc_binding
<222> 21430..21448
<223> potentialsite21449.mis1 potential
<220>
```

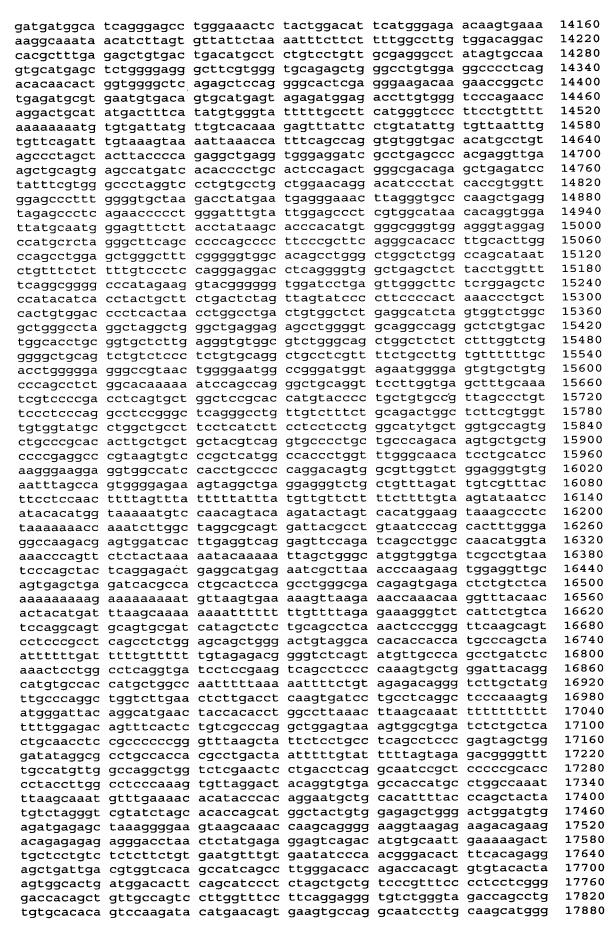
```
<221> misc binding
<222> 21450..21468
<223> complement potentialsite21449.mis2 potential
<220>
<221> misc_binding
<222> 21432..21450
<223> potentialsite21451.mis1 potential
<220>
<221> misc binding
<222> 21452..21470
<223> complement potentialsite21451.mis2 potential
<220>
<221> misc binding
<222> 21435..21453
<223> potentialsite21454.mis1 potential
<220>
<221> misc_binding
<222> 21455..21473
<223> complement potentialsite21454.mis2 potential
<220>
<221> misc_binding
<222> 21436..21454
<223> potentialsite21455.mis1 potential
<220>
<221> misc binding
<222> 21456..21474
<223> complement potentialsite21455.mis2 potential
<220>
<221> misc binding
<222> 21550..21568
<223> potentialsite21569.mis1 potential
<220>
<221> misc_binding
<222> 21570..21588
<223> complement potentialsite21569.mis2 potential
<220>
<221> misc_binding
<222> 21664..21682
<223> potentialsite21683.mis1 potential
<220>
<221> misc binding
<222> 21684..21702
<223> complement potentialsite21683.mis2 potential
<220>
<221> misc_binding
<222> 21675..21693
<223> potentialsite21694.mis1 potential
<220>
<221> misc_binding
<222> 21695..21713
<223> complement potentialsite21694.mis2 potential
```

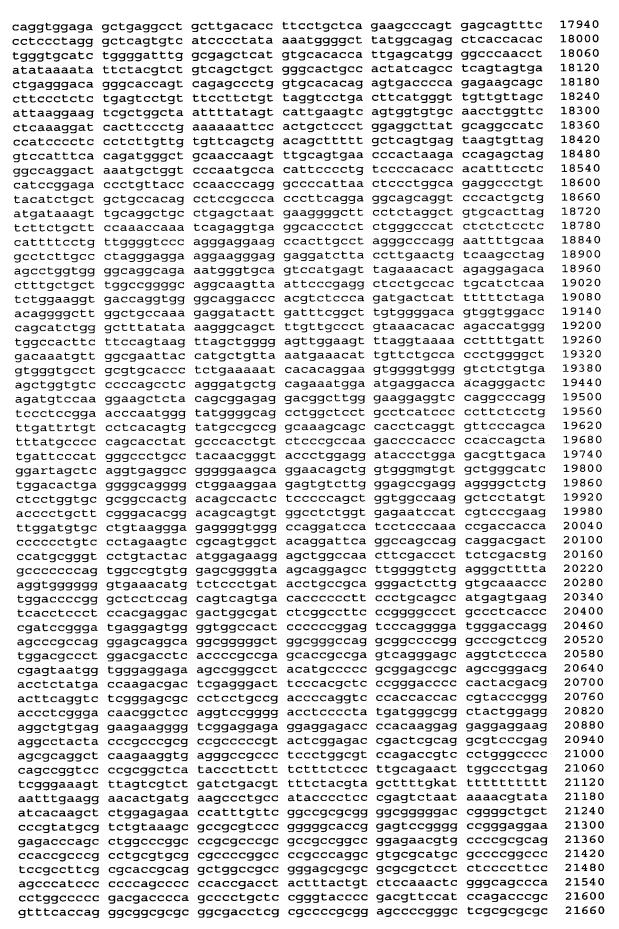
```
<220>
<221> misc binding
<222> 21709..21727
<223> potentialsite21728.mis1 potential
<220>
<221> misc_binding
<222> 21729..21747
<223> complement potentialsite21728.mis2 potential
<220>
<221> misc feature
<222> 22113,22122,22227,22264,22268
<223> n=a, q, c or t
<400> 1
                                                                       60
ccataatcaa gaaaatggat aataagtttt ggtggggatg tggagaaatt ggaatcctcc
gtgcattgct ggtgggaatg tacaatagtg cagtcattgg ggaaaacagt ttggcagttc
                                                                      120
ctcaaaaggt taaaaataga actaccaagt cacccagcaa ttccattctt aggcatatat
                                                                      180
tcaaaagaaa tgaaagcaga tatttgtaca ccagtgttca cagctgcact atttacaata
                                                                      240
gtcaaaaggt agaaacaacc taggtccatc cacaaatgaa tggataaata aaacgtagca
                                                                      300
                                                                      360
tatacataca atggtacact agtccgctgt aaaaagaaat tttgatctta ctgcatgcta
                                                                      420
catggcttcg acatactaca acatggatgg accttgaaaa cattattctt tgtgaaataa
                                                                      480
actagacaca ggacaaatgt tagacgattc cacttatatg aggcacctag aatgggcaat
ttggtaagca aagtagaata gaaattacta ggggcacagg tagcagggaa tggggagtta
                                                                      540
ctgtttaatg gtcacagagt ttatgttggg gatgatgaaa cagtttcggg gataaagagt
                                                                      600
ggtgactggt acacgacatt gtgaatatac ttaatgccac tgaattttac acttgaagtg
                                                                      660
                                                                      720
gttaaagcga taaatattat agtttgcata ttttatcata aaaatatttt tttaaacgat
                                                                      780
gaagggacgt gaacgggttg aaattttata aaaagtggcc agggaaggtg tcactgcaat
                                                                      840
ggtgtcctac aggaggagga agatcatgtg gacatctscg ggaagggtgt tctggcagag
                                                                      900
ggagtagcac gggcgatggc tctgaggact gtgagaagta tagttggaaa cagcgaggag
                                                                      960
qccaqqqtqt ccqaaqctqa qtaagccaga gagagtggga ggaggtgaga taagaggggg
                                                                     1020
aaggtcagtt tctgctgaga gtgaggagga gccacaggag ggctgtgagc aggtggacgt
gatctggctt gagttttaac agggccagta gaacaaagca cgcctgggta ccgaaaccag
                                                                     1080
ccactggcca gttggcaacc tgggggagtc taacgcgagg aagcgcccag ggttccccca
                                                                     1140
                                                                     1200
ggatgcgctt tccctcgccg ccacctggag acagcagagt cacgcccagc gctgcgcagg
ctgatcgccg cgccgcgccc ccgccctcgg tcgcaggtgg ctygttccgg gaattcctaa
                                                                     1260
gcggaaaccg gtcccaagcc ccgcgccttc gctcggcccc tttaagagcc agaatttccg
                                                                     1320
gagggctgac ccggggctag ggatgcccag gggccgaacc acaagttggg aacrggtggg
                                                                     1380
ggaggtggcg aaaacttccg wagtggaatt ccaacttttc ctggccctga ttccccttgg
                                                                     1440
gcatccctga gggggcagag cttcccttcc ggggacttta gagggttcct caggtcatct
                                                                     1500
aactgggaga cacaggaggc ccgaagcgcc cccctccac ccggtccgga ggaaccccag
                                                                     1560
                                                                     1620
tggaagtgga gaagtcaggc gccaccaaca agcctctccc agccaggact ttgcttagac
                                                                     1680
tegeteetee eggeagggeg cacetaggeg ggteeatege cageegggga gaggggtttg
                                                                     1740
ggcagggagg gaacaggtgc gcggcgggac ccgccctatc tcaacaggtg aatcgctcca
                                                                     1800
agtgggtctc ggttgcatgg atctcggtgc gcttggtttg gccggagmag atgggggccg
gaagggacct gtggtccgca ggcgccctcc cagcgggcca gtcacttggt tcgggccctg
                                                                     1860
ggggacggag cgcacctggg tcagcccact tccggggagg gaggcagagg aacccctccc
                                                                     1920
                                                                     1980
egeogeteae ceetaageee ageoetegge teccaecett gtgtacetgg geogaaceat
                                                                     2040
tcaccggagc gcgcagcggg tggagtgtgg ctcggaggac cgcggcgggt caagcacctt
                                                                     2100
tctcccccat atctgaaagc atgccctttg tccacgtcgt ttacgctcat taaaacttcc
                                                                     2160
agaatgcaac aggacggact tggagtaggg acaaggaacg gaagtgggaa ggggaggagc
                                                                     2220
gtgcacccct cctggccttg gtgcgcgccg cgcccctaa ggtactttgg aagggacgcg
cgggccagac gcgcccagac ggccgcgatg gcgctgttgg ccggcgggct ctccagaggg
                                                                     2280
                                                                     2340
ctgggctccc acccggccgc cgcaggccgg gacgcggtcg tcttcgtgtg gcttctgctt
                                                                     2400
agcacctggt gcacaggtac ggggcacggg gcctctgacg ctgcggaacg scggagggaa
ctgtagaggg ggatggatgg agttggaggc ggcgggaagc gggaagcggg ggtctcagag
                                                                     2460
gctgggacct tccgatcccc tgggtcttgg gcgatctgtt gcgcgcggga gtgagaggaa
                                                                     2520
ttccccattt gtgccgggga gcgctccccg cgcccttatc tggaagatag caggaagtga
                                                                      2580
                                                                      2640
aactccctgg acggtgagac ccggagcggc agggagaatg gaactctttg tggggaggga
                                                                      2700
gtggaagacc gcccgatctc tgggaaaaga aaagccggga tgggacttgg gcgcacccgg
ggatttctaa gttttggagt aacggggaga gggcacggga gggctggatc agacgcttcc
                                                                      2760
```

2820 tagagggaca gagacgaagg aacaatgcct aggcctcggg tgggtgtggg actggggact 2880 ccccatcccc cgcaccccac ccacctcccg cgggctccgg attatacgtg cgtaagagtc 2940 tqqtqqqatq qatttacgga cttgaaaccg acttctgctg gcaggctttc acctggatgg 3000 qatatttggg tggtgatgag gtctttcccg agacactttt ggttcagtca tttgaaatga ctttagagta gggtgaggtg gtgggaggct gatggagata ttgtgggggc tttagtccct 3060 ccatggcaaa gcagttcagg caaacaactc catggttttc cctccaaatt caaaaggccc 3120 3180 cgggtaacct ggaatccttc gtagtcggtt ttgaagtggg gccttgggcg ctgggggcat caacatggcc atctgggctt gcctgcccag gccacacaga ggccccttgt tgtgggtgaa 3240 tggcaaaggg aagaggggac tggtgtggtt cagaggccac aggctgggaa gagggatggc 3300 gggcgagtcc aaggaaactg gccgtgtcac cgtgcacctg ccacttcagc cccacgggtc 3360 tataaaatgg gcatgattat cgtggctacc tcactggtcc tggcaattaa ggaacaatgt 3420 gtgccaggca ctctgtaaac cacatacttg cgagtgtcaa gctggtgaca ggtggcgttc 3480 ctgttgaagc acctccctga gctcacagca acccttgctg tctctcctct tgccctcagc 3540 3600 tectqceaqq qecatecaqq tgacegtgte caacecetae caegtggtga tectetteca 3660 qcctqtqacc ctqccctqta cctaccagat gacctcgacc cccacgcaac ccatcgtcat 3720 ctggaagtac aagtetttet geegggaeeg categeegat geetteteee eggeeagegt 3780 cqacaaccaq ctcaatgccc agctggcagc cgggaaccca ggctacaacc cctacgtyga 3840 gtgccaggac agcgtgcgca ccgtcagggt cgtggccacc aagcagggca acgctgtgac cctgggagat tactaccagg gccggaggat taccatcacc ggaagtatgt tgggcagggc 3900 agggggatga ggctgggctt gcccgggtgg tgggactggc gtccttgtgc gggacctgga 3960 4020 gtccccatct gaaagctctt gagtgccagt gtctgaaagg accattgaag ggagcaattc ttttttttt ttttttgaa gatggagtct tgctctggac tccaggctgg agtgcagtgg 4080 tgcgatetea geteactgea acetecacet eccaggitea ageaattete tigeeteage 4140 ctcccgagta gctgggactc caggtgcgtg ccaccacgcc cagttaattt ttgtattttt 4200 agtagagatg gggtttcacc atgttggcca ggctggtctc aaactcctga cctcaaatga 4260 tctgcccgcc ttggcctcgc aaagtgctga gagacaccat acccagccta aagggagcga 4320 4380 tttttgagta cctgtcatat accaggtgct gttctgggcc ctgggaatac agctgttaac 4440 aaaatcatca aaccacttcc ctcgtggagc ccacattgca gtgagagaga caaacackac 4500 4560 acacactctc aagtccttga agataaagaa aactgggtaa cggagagaag aggccagggt 4620 ttgttctata atcattaata acacgagcag taagaagtaa aatttatcta agtaacaact 4680 tataaaqqqt ctactqtqtq ctaagctctc atccaggttc ccaaggatta actcagacca 4740 cacagtaatt gaatagattc tatcattgtc atcttacaga ggcccagaga gagaaagtga 4800 cttgcctagt gtcatagctg gtaacggggc tgggattcta actcagccac tttgggtcta 4860 qtqqccaaqc tcctaatccc tttgcttgcc tagggtggtc cgcagaggac tcacagagga gatggcagga gtgaactgca ggggcaagag agcttaatgg agaaagcctg tgacatgcca 4920 ggaactgcac acatattctc ccattgagtc ctctcctcta ccctcctgac agctgaggca 4980 5040 cagagaggtt accttgttca aatgggtgca taggaagtca aagtctggag ctggggtttg aacccaggca gccctgagaa ccttgttctt tttttttgag acggagtctc gctctgtcgc 5100 5160 ccaggetgga gtgcagtggc gggatetegg etcaetgcaa geteegeete eegggtteae gccattctcc tgcctcagcc tcccaagtag ctgggactac aggcgcccgc cactacgcct 5220 ggctaatttt ttgtattttt agtagagacg gggtttcacc gttttagccg ggatggtctc 5280 gatotoctga cotogtgato ogocogocto ggootoccaa agtgotggga ttacaggogt 5340 gagccaccgc gcccggcccc ttgttcttaa ctgtaatgct gcctcctgat aggatgtgcc 5400 tgttgggact aagtaagggg cagtcattca ttcattcatt tggtatttat caagcatcga 5460 ctatgtgtcg ttggtgctgg ggatagaggt gattgggatg gctgaagttt ctgtcgtcaa 5520 ggagatgaca ttctggtgga gtgagactgg cagtaaataa gcagataaag aaagagtatg 5580 agaatttcaa agtctgggca cggtggctca cgtctgtaat ctcagcactt tgggaggcca 5640 5700 aggtgggtgg atcacctgag gtcaggagtt ccagaccagc ctggccaaca tggtgaaacc 5760 ccgtctctac taaaaataca aagattagcc aggcatggtg gcacatgcct gtaatcccag 5820 ctactcagga ggctgaggca tgagaatcgc ttgaacccag gaggcagagg ttgcagtgag 5880 ctgagatcgc accactgtac tgcagtctgg gcgacagagt gagactctgt ctcaaaaaaa 5940 aaaaaaaaaa aaaagactcc gtcaaggtat aagaatgtca gagagtacta agtgttgcaa 6000 agaaaataac accaggctgg gtgcattggc tcatgcctgt aaatttcagc actttgggag 6060 gccaaggcag gaggatcact tgagcctagg agtttgagac cagcctggac aacaaaatga gaccccatgt ctacaaaaat tttaaaaatt taaaaattag ctgggcatgg tggcatgtgc 6120 6180 ctgtggtccc ggctgctcag gaggctgagg tgggaggatt gcttgggctt gagaggtcaa 6240 ggcttcagtg agtcatgatc gtgccactgc attccagcct gggtgacaga gtgagaccct 6300 gtcttgaaat gaaaagaaaa taggctgggc gcagtggctc acacctgtaa tcccagcact ttgggaggcc gaggtgggtg gatcacctga ggtcaggaga tcgagaccag cctggccaac 6360 atggtgaaat cccatctcta ctaaaaatac aaaatttagc cgggcgtggt ggtgggcgcc 6420 6480 tgtaatccca gctactcggg aggctgaggc aggagaatcg cttgaacctg ggaggcgaag gttgcggtgc gccaagattg cgccactgca ctctagcctg ggaaacagtg agactccgtc 6540



ttaggattac aggtgtgagc caccatgtcc ggccaagagg gtgttcattt ctgctccttg 10380 ccaggtattg tgtcaggcac tggggaccca gcagtggctg agacagacag ggctctgcct 10440 10500 cacggagccc acattttcac caggcaaagg atggtcggcc cctaagctgg gagataagac 10560 ttcagcagtt gggtgggga gccgtgggag aagcccagcc cacaggggga cagtgcaaat ctagaaccaa ggcgatggca ggggtgaggc tggcacggta gctagagacc acgtcgtgcc 10620 10680 aagggccttg gggaccatgg gactatggga ccttagggaa ggcgtctgga atgctgtagc 10740 cagacactgt tgcaaggagg atttttctgt agacatgagg ccttccttat gaagaaagca 10800 agggttcttt cattcctggg ggtgccaggt gctgtggact gcagcacgcg tggttgctgc cgtcacagag ctgtcatgca ggagggcagc gcgtccttgg gaaggtggca ggcaggtcag 10860 gctaggagga aagaggccgg gaagctgagg gcatttcctg cccgagatgc ccaatgtagc 10920 10980 ctacttctgt ccccagtggc ttaaggcaga gttgcctggt aggtgccctg gtcccaccct ggtgaaaggc tgaaggtatt taattagtgc ctgagaagca gagaggaaac aggatgtgcc 11040 aaaacacttt gatggatggt agagttaaca ggctccttgc ctgcagctgc ttcagacaag 11100 agcgtcccca agccctgggc ctgacctgga atgtggggat ggaaggggag ggggaggaac 11160 11220 caaggcactg ggagggtaag tetetetete ecacatagae acacecaete ettatgggtg 11280 cctgggcatc tcctggtacc tagaatctgg cctgtttatc tccacaccca tccctggggt 11340 ctacactagg ccctgtgggt ggcagttcac atcaggggag ttctgacttt ggctctgaga ggtggttcag agatggctgt aagttgagaa gcacagactg ctgggtgtgg tggttcacgc 11400 ctgtaatccc agcactttgg gaggctgagg tgggggtgga tcacctgagg tctggagttc 11460 aaaaccaact tggtcaacat ggcgaaactc catctctact aaaaatgcaa aaattagcca 11520 11580 ggtgtggtgg caggtgccta taatcccagc tacatgggag gctgaggcag gagaatcgct tgaatctggg aggcgaagat tgtagtgagc cgagattagt tcgcaccatt gcatgccagc 11640 ctgggcaaca agagtgaaac tccgattcaa acaaacaaaa aaaaaaagct gggcatggtg 11700 11760 gagtgcctgt agtcctaact actcaggtgg gaggattgct tgagtccagg aggttgaagt 11820 tgcagtgggc tataattaca ccactgcact ccagccaggg ccacagagtg agaccctgtc tctaaagaaa gaaaaaaaaa aacaacctca ggctccgagg gcaccattac tgctctacac 11880 tgaagagctg tgcagctttt ccagacccga aatgtcatcc acaaaacaga agtgataatg 11940 qtcctqcctc acagacttct tgcagtagtc caggtgttta gaacggggtg taaaaggccg 12000 tgtgcccttg gtaggaatct ttgcatatgc atttgatcat ctgcagcctg cccagcccac 12060 tgcttgcccc ctcctgggtg tgctgggaag gggtctttgg ccctccaggg gttaggtgcc 12120 ccagcctcca aggtgccctc acgccttttc atcccgactc agatgctgac ctgacctttg 12180 accagacggc gtggggggac agtggtgtgt attactgctc cgtggtctca gcccaggacc 12240 tccaggggaa caatgaggcc tacgcagagc tcatcgtcct tggtgagtgg gcctgggaag 12300 12360 cetetgeect ceagettace etetgggete tgtegeetge tetgetetee eecaggetet 12420 12480 gccagtcact taggctcccc tgtgccctgc accccaggca gggaccactg gcccacagtg cctccaatca cccaagccaa actaagagaa gagtggagac aattggagac tctgcctttt 12540 12600 caaagtctca tttttaaaaa aaatccagac ttggggtccg ggtgcggtag ttcatgcctg 12660 taatcccagc actttgggag gccgaggcgg gtggatcact tgaggccagg agttcgagac tagcctggcc aacgtggcaa aatcccgtct ctataaaaaa tataaaagcc aggcgtggtg 12720 12780 gtgcacatgc ctgtaatccc agttactcag aaggctgagg catgaggatt gcttgaacct gggaggcaga ggatgcagta agccaagatc aagccactgc actccagcct gggcgacaga 12840 gtgagactct gtccaaaaaa aaaaaaaatc cagacgtggt cagagtccat gggcagtgaa 12900 tgaggacagt tgatggtgtg caaaatcgac ccacctcttg ctacatcccc aaggcctcat 12960 13020 ctcacccgag tccctcgcca aagcacagcg gttttgccgt gtgccctgct gggatggcgc tgcatggcac acacactgtg taagtttgag tgcagctgaa acgaagccga ttccagacac 13080 ccaggggcag ggcggggtgt ccgtgtggct gggaggcctc cttgtgttag ggggatgttg 13140 ccatcggcca ggtgccctgc tgtaagccaa cacatggagt cttgtatgac atgtgctctg 13200 13260 catgagtgat gccgctgggc tgtacactgc catcttcaca tgtgtgaatg agcacgtgac 13320 tqqqqqtac ttqggctgca agacagagtt catgtgtggg ggatggaaca cgtgcaccag tgacccagga acctctgcct gttcttcggt aaaatgcacc atttgcatca gcagttccca 13380 13440 aaattagtct ccaggtctat ttacactcta aaacattatc gagggtctcc aagagctttt gtttgtttct gtgggtttta tgtctatctg ttgcttaaca tattaggaat taaaatgggg 13500 agattttcct ttttttttt tttttttga gatggagtct cgttctgtcg cccaggctgg 13560 agtgcagtgg ctcgatctcg gctcactgca agcttcacct cctgggttca cgccattctc ctgcctcagc ctcccaagta gctgggacta caggcacccg ccaccacacc cggctaattt tttttgtatt tttagtagag actgggtttc accatgttag ccaggatggt ctcgatctcc 13740 tgacctcgtg atccacccac ctgggcctcc caaagtgctg ggattacagg catgagccac 13800 tgcccggcct taaaatgggg agatttttca agcccaagat acacaaggaa gactgggcaa 13860 catggcaaga ccctgactct acaaaaaatt ttaaaattaa ccaggcatgg tggcatgcac 13920 ctgtgagccc agcttcttgg gaggctgagg caggagtatc gcttgcaccc aggaggtcaa 13980 14040 ggctgcagtg agccatgact atgctactgc actctagcat gagtgacaga gaccctggct 14100 caagaaacac aaacacacac acacacacac acacgcatat agtccattag gcatcagggc





```
ccgcccgccc ccggagacag acagcgcgcg cgctcccggg ccgcctcccc ccagcgcgcg
teegeeeegg getegegeeg eegeegeege egeegeege egegegeage teaagtaaag
gaggaaaaaa aaaaggggga aaaatagaaa gcggcggcgg ctgcagcagc gatccgccgc
                                                                  21840
                                                                  21900
cggactgggc caagccgggc ggcggccgcg cgagccggcg atccagggca ctggcggcgg
                                                                  21960
ccagccaggg cgggccgtgt tcaaaaaaaa aagtcgcggc ggcggcggct gctcagggaa
ggaggcctga gggccgcgtg cagcgggcgg gcagctgggt gggctggggg cggccgcgcg
                                                                  22020
                                                                  22080
gcgtcccgga gcctcgggcc gcccggagcc ggcgggcggg cggaggcgga ggcggcggcg
gctgcagcgg ctgcaggagc ggcggcggct gcngcggcgg cngcggcatc tcctcctcac
                                                                  22140
atgaccccac tgtttgtccc cgtgatcagc gcgagcggct cccgtatctc ctccgtcccc
                                                                  22200
tectgeegeg eggegtgage geegggnete ggggeeeeee eggeegeeeg eeeeeteeee
                                                                  22260
                                                                  22320
teenteente eceteceete eceteceece egggeecege geecececeg ececegecee
ccccatggac atgctggacc cgggtctgga tcccgctgcc tcggccaccg ctgctgccgc
cgccaggtaa gatccccggc ccggccgtgc ccccgcgccc cggccccggc cccggccccg
cggcctgcag gccggggccg ccatgatccc gagcggccgc gggccccgct caaaatggag
gccgccggcg cggggggac ctggcgcctc ccgccccgg cccccggcct cggcggcgcc
                                                                  22620
cccggcctca ggcgcggccg ggtgggactg gggccctgca gctgggcgcg ggggcggggg
                                                                  22680
cgcgggcgcg ggccgcgctg accetgctcc ctcctgtgcc cctggcagcc acgacaaggg
                                                                  22740
accogaggcg gaggaggcg togagctgca ggaaggtgag tgcttgccgg gccggccgcg
cccggggagg gctgggggg ctcggcgcgg ccctgaccgt gccccgaccc tcctcggccc
                                                                  22800
                                                                  22860
caggegggga eggeceagga geggaggage agacageggt ggecateace agegtecage
aggcggcgtt cggcgaccac aacatccagt accagttccg cacagagaca aatggaggac
                                                                  22920
aggtgagcgg cgggccgcga gagcgaacgg gcggcgggc gggcgcgccg ggaaggctcg
                                                                  22980
gacctggccc cagcgccggc ctcgccgctc tgccgccccc tgcaggtgac ataccgcgta
                                                                   23040
gtccaggtga ctgatggtca gctggacggc cagggcgaca cagctggcgc cgtcagcgtc
                                                                   23100
gtgtccaccg ctgccttcgc gggggggcag caggctgtga cccaggtggg tgtggacggg
                                                                   23160
                                                                   23187
gcagcccagc gcccgggccc cgccgct
<210> 2
<211> 2158
<212> DNA
<213> Homo sapiens
<220>
<221> allele
<222> 595
<223> 9-3-324 : polymorphic base C or
<220>
<221> allele
<222> 940
<223> 9-6-187 : polymorphic base C
<220>
<221> allele
<222> 1191
<223> 9-7-325 : polymorphic base A
<220>
<221> allele
<222> 1362
<223> 9-9-246 : polymorphic base G or C
<220>
<221> allele
<223> LSRX9f13-BM : polymorphic base deletion of AGG
<220>
<221> allele
<222> 2079
<223> LSRX9f14-BM : polymorphic base T or G
<400> 2
```

														+ - + -		: 60
tggag atgcc	gtgt	gg c	tcgg	jagga	C CG	cggc	gggt	caa +	gcac	tcc	2020	eccc	at a	cad	gaaago	115
atgee	CCC	ig i	ccac	greg	,	acgo	ccac	. Laa	.aact		aya		Gln			113
gga c	ett	qqa	qta	aga	aca	agg	aac	qqa	agt	ggg	aag	ggg	agg	agc	gtg	163
Gly I																
5.		- 1		1	10	5		1		15	-	-	_		20	
cac c	200	taa	t.aa	cct		tac	aca	cca	cac	ccc	cta	agg	tac	ttt	qqa	211
His F	oro	Ser	Trn	Pro	Trp	Cvs	Ala	Pro	Ara	Pro	Leu	Ara	Tvr	Phe	Glv	
1110 1		JCI	112	25		0,0			30			5	- 4 -	35	- 4	
agg g	Tac	aca	caa		aga	cac	acc	cag		acc	aca	atq	aca	cta	tta	259
Arg A	gac Nen	712	Arg	Ala	Ara	Ara	Δla	Gln	Thr	Δla	Δla	Met	Ala	Leu	Leu	
Arg F	rsp	AIG	40	AIA	AL 9	AL 9	AIG	45		1114			50			
gcc s	777	aaa		tac	3073	aaa	cta		tcc	cac	cca	acc		gca	aac	3 0 7
Ala	395 217	G1 v	Leu	Cor	Ara	232	Len	Glv	Ser	His	Pro	Δla	Δla	Δla	Glv	
AIA C	эту	55	пси	SCI	Arg	Cly	60	Cly	001	1110	110	65			~- <i>1</i>	
cgg g	~~~		ata	ata	++0	ata		ctt	cta	ctt	agc		taa	tac	aca	355
Arg A	yac Nan	712	y.c.	y.l	Dho	y - 9	Trn	Len	I.eu	T.eu	Ser	Thr	Trn	Cvs	Thr	333
	70	Ата	vai	vai	PHE	75	пр	Бец	пси	пси	80	1111	TTP	Cyb	1111	
gct o	. •	~~~	200	~~~	2 + 4		ata	200	ata	tcc		CCC	tac	cac	ata	403
Ala	Dage	710	ayy	712	TIO	Clay	yra1	Thr	y - 1	Cor	Agn	Pro	Tur	Hic	Wal	105
	PLO	Ala	Arg	Ala	90	GIII	vaı	TIIT	vaı	95	ASII	FIO	тут	1113	100	
85						~		a+~	~~~		200	+ 2.0	a2a	ata		451
gtg a	atc	CCC	Db-	cag	Desc	grg	acc	Lou	Dvo	Cura	Thr	Tur	Cla	Mo+	Thr	431
Val I	тте	Leu	Pne		Pro	vai	THE	ьeu	110	Cys	1111	TAT	GIII	115	1111	
				105						224	+	224	t a t		taa	499
tcg a																493
Ser :	rnr	Pro		GIn	Pro	тте	vaı		Trp	гув	TYL	цуѕ		Pne	Cys	
			120					125					130			E 4 77
cgg g	gac	cgc	atc	gcc	gat	gcc	ttc	tcc	ccg	gcc	agc	gtc	gac	aac	cag	547
Arg A	Asp		Ile	Ala	Asp	Ala		Ser	Pro	Ата	ser		Asp	Asn	GII	
		135					140					145				-05
ctc a	aat	gcc	cag	ctg	gca	gcc	<u>a</u> aa	aac	cca	ggc	tac	aac	CCC	tac	gty	595
Leu I		Ala	Gln	Leu	Ala		Gly	Asn	Pro	GIA		Asn	Pro	Tyr	vaı	
	150					155					160					
gag	tgc	cag	gac	agc	gtg	cgc	acc	gtc	agg	gtc	gtg	gcc	acc	aag	cag	643
Glu (Cys	Gln	Asp	Ser		Arg	Thr	Val	Arg		Val	Ala	Thr	ГÀг		
165					170					175					180	
ggc a	aac	gct	gtg	acc	ctg	gga	gat	tac	tac	cag	ggc	cgg	agg	att	acc	691
Gly 2	Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr		Gln	Gly	Arg	Arg		Thr	
				185					190					195		
atc a	acc	gga	aat	gct	gac	ctg	acc	ttt	gac	cag	acg	gcg	tgg	999	gac	739
Ile '	Thr	Gly	Asn	Ala	Asp	Leu	Thr		Asp	Gln	Thr	Ala		GIA	Asp	
			200					205					210			
aģt (787
Ser	Gly		Tyr	Tyr	Cys	Ser			Ser	Ala	GIn		Leu	GIn	GLY	
		215					220					225				
aac	aat	gag	gcc	tac	gca	gag	ctc	atc	gtc	ctt	<u>aaa</u>	agg	acc	tca	ggg	835
Asn .	Asn	Glu	Ala	Tyr	Ala		Leu	Ile	Val	Leu		Arg	Thr	Ser	GIY	
	230					235					240					
gtg																883
Val .	Ala	Glu	Leu	Leu	Pro	Gly	Phe	Gln	Ala	Gly	Pro	Ile	Glu	Asp		
245					250					255					260	
ctc	ttc	gtg	gtt	gtg	gta	tgc	ctg	gct	gcc	ttc	ctc	atc	ttc	ctc	ctc	931
Leu	Phe	Val	Val	Val	Val	Cys	Leu	Ala	Ala	Phe	Leu	Ile	Phe			
				265					270					275		
ctg	ggc	aty	tgc	tgg	tgc	cag	tgc	tgc	ccg	cac	act	tgc	tgc	tgc	tac	979
Leu	Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	
			280					285					290			
gtc																1027
Val	Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys			Ala	Leu	
		295					300					305				_
tat	gcc	gcc	ggc	aaa	gca	gcc	acc	tca	ggt	gtt	CCC	agc	att	tat	gcc	1075
Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	

	310					315					320					
ccc		acc	tat	acc	cac	ctg	tct	ccc	qcc	aaq		cca	ccc	сса	cca	1123
						Leu										
325					330					335					340	
						cct										1171
Ala	Met	Ile	Pro		Gly	Pro	Ala	Tyr		Gly	Tyr	Pro	Gly		Tyr	
				345					350					355	+-+	1219
cct	gga	gac	gtt	gac	agg	art	agc	Com	gct	ggt	ggc	Cla	ggc	Cor	Tur	1219
Pro	GTA	Asp	360	Asp	Arg	Xaa	ser	365	Ala	GTA	СТУ	GIII	370	Ser	ıyı	
ata	ccc	cta		caa	aac	acg	gac		agt	ata	acc	tct		atc	cac	1267
Val	Pro	Lei	Len	Ara	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val	Arq	
var	110	375		5			380					385			_	
aqt	ggc		agg	att	cag	gcc	agc	cag	cag	gac	gac	tcc	atg	cgg	gtc	1315
Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Ser	Gln	${\tt Gln}$	Asp	Asp	Ser	Met	Arg	Val	
	390					395					400					
ctg	tac	tac	atg	gag	aag	gag	ctg	gcc	aac	ttc	gac	cct	tct	cga	cst	1363
	Tyr	Tyr	Met	Glu		Glu	Leu	Ala	Asn		Asp	Pro	Ser	Arg	хаа 420	
405		~~~	-~+	~~~	410	gtg	a . a	aaa	acc	415	aat	ass	atc	acc		1411
ggc	Dro	Dro	cor	ggc Glv	Ara	Val	Glu	Δra	Δla	Met	Ser	Glu	Val	Thr	Ser	1111
GIY	FIO	FIO	DCI	425	n. 9	Vul	Olu	****9	430		001			435		
ctc	cac	qaq	qac		tgg	cga	tct	cqq		tcc	cgg	ggc	cct	gcc	ctc	1459
Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	Pro	Ser	Arg	Gly	Pro	Ala	Leu	
			440					445					450			
acc	ccg	atc	cgg	gat	gag	gag	tgg	ggt	ggc	cac	tcc	CCC	cgg	agt	CCC	1507
Thr	Pro		Arg	Asp	Glu	Glu		Gly	Gly	His	Ser		Arg	Ser	Pro	
		455					460					465	~~~	~~~	+~~	1555
agg	gga	tgg	gac	cag	gag	ccc Pro	gcc	agg	gag	Cag	gca	ggc	999 Glv	ggc Glv	Trn	1555
Arg	470	Trp	Asp	GIN	GIU	475	Ата	Arg	Gru	Gili	480	Gry	GIY,	Gry	пр	
caa		agg	caa	CCC	caa	gcc	cac	t.c.c	ata	gac		cta	qac	qac	ctc	1603
Ara	Ala	Ara	Ara	Pro	Ara	Ala	Arq	Ser	Val	Asp	Ala	Leu	Asp	Asp	Leu	
485			_		490		J			495					500	
acc	ccg	ccg	agc	acc	gcc	gag	tca	ggg	agc	agg	tct	CCC	acg	agt	aat	1651
Thr	Pro	Pro	Ser	Thr	Ala	Glu	Ser	Gly	Ser	Arg	Ser	Pro	Thr		Asn	
				505					510					515		1.000
ggt	aaa	aga	agc	cgg	gcc	tac	atg	CCC	ccg	cgg	agc	cgc	agc	cgg	gac	1699
GIY	GIY	Arg	520	Arg	Ата	Tyr	мес	525	Pro	Arg	Ser	Arg	530		Asp	
aac	ctc	tat		саа	gac	gac	tca		gac	ttc	cca	cac			gac	1747
Asp	Leu	Tvr	Asp	Gln	Asp	Asp	Ser	Arq	Asp	Phe	Pro	Arg	Ser	Arg	Asp	
		535					540		•			545		_	_	
ccc	cac	tac	gac	gac	ttc	agg	tct	cgg	gag	cgc	cct	cct	gcc	gac	CCC	1795
Pro	His	Tyr	Asp	Asp	Phe		Ser	Arg	Glu	Arg			Ala	Asp	Pro	
	550					555					560					1043
															agg	1843
_		His	His	His	Arg 570		Arg	Asp	Pro	575		ASII	. Сту	261	Arg 580	•
565		. cac	ctc	ccc			aaa	caa	cta			gag	act	ata	agg	1891
Ser	. Glv	Asp	Leu	Pro	Tvr	Asp	Glv	Ara	Leu	Leu	Glu	Glu	Ala	Val	Arg	
	1	P		585		_	-	J	590					595		
aag	aag	999	tcg	gag	gag	agg	agg	aga	ccc	cac	aag	gag	gag	gag	gaa	1939
Lys	Lys	Gly	Ser	Glu	Glu	Arg	Arg	Arg	Pro	His	Lys	Glu	Glu	Glu	Glu	
			600					605					610			1007
gag	gcc	tac	tac	ccg	CCC	gcg	ccg	CCC	ccg	tac	tcg	gag	acc	gac	tcg	1987
Glu	ı Ala			Pro	Pro	АІА	620		PTC	туг	ser	625		ASP	Ser	
Cac	ı acc	615 tcc		gan	י כמי	add			aao	aac	tta			raαt	cgg	2035
Glr	Ala Ala	Ser	Aro	Glu	Aro	Ara	Leu	Lvs	Lvs	Asn	Leu	Ala	Leu	Ser	Arg	•
	630		3	,	5	635		~			640				_	
gaa	agt	tta	gto	gto	tga	tct	gacg	ttt	tcta	cgta	ıgc t	tttg	katt	t		2083
Glu	. Ser	Leu	Val	. Val	. *											

290

650 645 ttttttttaa tttgaaggaa cactgatgaa gccctgccat acccctcccg agtctaataa 2143 2158 aacgtataat cacaa <210> 3 <211> 649 <212> PRT <213> Homo sapiens <220> <221> VARIANT <222> 363 <223> 9-7-325 : polymorphic amino acid Ser or Asn <220> <221> VARIANT <222> 420 <223> 9-9-246 : polymorphic amino acid Pro or Arg <220> <221> VARIANT <222> 519 <223> LSRX9f13-BM : polymorphic amino acid deletion of Arg <400> 3 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 10 Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu . 20 25 Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala 40 Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro 55 Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser 70 75 Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn 85 -90 Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr 105 Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr 120 Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser 135 140 Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr 155 150 Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val 170 165 Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly 185 Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr 200 Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln 215 Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly 235 Arg Thr Ser Gly Val Ala Glu Leu Leu Pro Gly Phe Gln Ala Gly Pro 245 Ile Glu Asp Trp Leu Phe Val Val Val Cys Leu Ala Ala Phe Leu 265 Ile Phe Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr 280 Cys Cys Cys Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys

300

295

<220>

<221> allele <222> 1134

```
Pro Glu Ala Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro
                                       315
                   310
Ser Ile Tyr Ala Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr
                                  330
              325
Pro Pro Pro Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr
                               345
Pro Gly Gly Tyr Pro Gly Asp Val Asp Arg Ser Ser Ser Ala Gly Gly
                          360
Gln Gly Ser Tyr Val Pro Leu Leu Arg Asp Thr Asp Ser Ser Val Ala
                       375
Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Ser Gln Gln Asp Asp
                                      395
                   390
Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp
                                   410
               405
Pro Ser Arg Pro Gly Pro Pro Ser Gly Arg Val Glu Arg Ala Met Ser
                               425
Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg
                           440
                                              445
Gly Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Gly Gly His Ser
                       455
                                          460
Pro Arg Ser Pro Arg Gly Trp Asp Gln Glu Pro Ala Arg Glu Gln Ala
                   470
                                       475
Gly Gly Gry Arg Ala Arg Arg Pro Arg Ala Arg Ser Val Asp Ala
               485
                                   490
Leu Asp Asp Leu Thr Pro Pro Ser Thr Ala Glu Ser Gly Ser Arg Ser
                               505
Pro Thr Ser Asn Gly Gly Arg Ser Arg Ala Tyr Met Pro Pro Arg Ser
                                               525
                           520
Arg Ser Arg Asp Asp Leu Tyr Asp Gln Asp Asp Ser Arg Asp Phe Pro
                                          540
                       535
Arg Ser Arg Asp Pro His Tyr Asp Asp Phe Arg Ser Arg Glu Arg Pro
                                      555
                  550
Pro Ala Asp Pro Arg Ser His His His Arg Thr Arg Asp Pro Arg Asp
               565
                                   570
Asn Gly Ser Arg Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu
                               585
Glu Ala Val Arg Lys Lys Gly Ser Glu Glu Arg Arg Pro His Lys
                           600
                                              605
Glu Glu Glu Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser
                                           620
                        615
Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu
                    630
                                        635
Ala Leu Ser Arg Glu Ser Leu Val Val
                645
<210> 4
<211> 2101
 <212> DNA
<213> Homo sapiens
<220>
<221> allele
<222> 595
 <223> 9-3-324 : polymorphic base C or T
<220>
 <221> allele
 <222> 883
 <223> 9-6-187 : polymorphic base C or T
```

<223> 9-7-325 : polymorphic base A or G	
<220> <221> allele <222> 1305 <223> 9-9-246 : polymorphic base G or C	
<220> <221> allele <222> 1601 <223> LSRX9f13-BM : polymorphic base deletion of AGG	
<220> <221> allele <222> 2022 <223> LSRX9f14-BM : polymorphic base T or G	
<pre><400> 4 tggagtgtgg ctcggaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc atgccctttg tccacgtcgt ttacgctcat taaaacttcc aga atg caa cag gac</pre>	60 115
gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agg agc gtg Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val 5 10 15 20	163
cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly 25 30 35	211
agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg Arg Asp Ala Arg Ala Arg Ala Gln Thr Ala Ala Met Ala Leu Leu 40 45 50	259
gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Gly 55 60 65	307
cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr 70 75 80	355
gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val 85 90 95 100	403
gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Thr 105 110 115	451
tcg acc ccc acg caa ccc atc gtc atc tgg aag tac aag tct ttc tgc Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys 120 125 130	499
cgg gac cgc atc gcc gat gcc ttc tcc ccg gcc agc gtc gac aac cag Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln 135 140 145	547
ctc aat gcc cag ctg gca gcc ggg aac cca ggc tac aac ccc tac gty Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val 150 155 160	595
gag tgc cag gac agc gtg cgc acc gtc agg gtc gtg gcc acc aag cag Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln 165 170 175 180	643
ggc aac gct gtg acc ctg gga gat tac tac cag ggc cgg agg att acc Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr 185 190 195	691
atc acc gga aat gct gac ctg acc ttt gac cag acg gcg tgg ggg gac Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr Ala Trp Gly Asp 200 205 210	739
agt ggt gtg tat tac tgc tcc gtg gtc tca gcc cag gac ctc cag ggg Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Gln Gly	787

		215					220					225				
aac	aat		acc	tac	gca	gag		atc	atc	ctt	qac		ctc	ttc	gtg	835
Asn	Asn 230	Glu	Ala	Tyr	Ala	Glu 235	Leu	Ile	Val	Leu	Asp 240	Trp	Leu	Phe	Val	
qtt	gtg	gta	tgc	ctg	gct	gcc	ttc	ctc	atc	ttc	ctc	ctc	ctg	ggc	aty	883
Val	Val	Val	Cys	Leu	Ala	Ala	Phe	Leu	Ile	Phe	Leu	Leu	Leu	Gly	Ile	
245					250					255					260	
tgc	tgg	tgc	cag	tgc	tgc	ccg	cac	act	tgc	tgc	tgc	tac	gtc	agg	tgc	931
-				265		Pro			270					275		
CCC	tgc	tgc	cca	gac	aag	tgc	tgc	tgc	CCC	gag	gcc	ctg	tat	gcc	gcc	979
			280			Cys		285					290			
ggc	aaa	gca	gcc	acc	tca	ggt	gtt	CCC	agc	att	tat	gcc	CCC	agc	acc	1027
		295				Gly	300					305				
tat	gcc	cac	ctg	tct	CCC	gcc	aag	acc	cca	ccc	cca	cca	gct	atg	att	1075
_	310					Ala 315					320					
ccc	atg	ggc	cct	gcc	tac	aac	ggg	tac	cct	gga	gga	tac	cct	gga	gac	1123
Pro	Met	Gly	Pro	Ala	Tyr	Asn	Gly	Tyr	Pro		Gly	Tyr	Pro	Gly		
325					330					335					340	
gtt	gac	agg	art	agc	tca	gct	ggt	ggc	caa	ggc	tcc	tat	gta	CCC	ctg	1171
				345		Ala			350					355		1010
ctt	cgg	gac	acg	gac	agc	agt	gtg	gcc	tct	gaa	gtc	cgc	agt	ggc	tac	1219
			360			Ser		365					370			1267
agg	att	cag	gcc	agc	cag	cag	gac	gac	tcc	atg	cgg	gtc	ctg	tac	tac	1267
		375				Gln	380					385				1215
atg	gag	aag	gag	ctg	gcc	aac	ttc	gac	CCT	tct	cga	CST	ggc	Desc	Dwo	1315
	390					Asn 395					400					1262
agt	ggc	cgt	gtg	gag	cgg	gcc	atg	agt	gaa	gtc	acc	CCC	CTC	cac	gag	1363
		Arg	Val	Glu		Ala	Met	Ser	GIU			ser	Leu	HIS	420	
405					410					415		ata	200	999		1411
gac	gac	tgg	cga	tct	cgg	cct	tcc	cgg	ggc	CCL	gcc	TOU	Thr	Dro	Tle	1411
_				425		Pro			430					435		1459
cgg	gat	gag	gag	tgg	ggt	ggc	cac	Cox	D~0	222	agu	Dro	ayy Ara	Glv	Trn	1437
			440			Gly		445					450	-		1507
gac	cag	gag	D~o	315	ayy	gay	Cay	۸la	Glv	999	Glv	Trn	- Δra	Δla	agg Arg	130.
Asp	GIII			Ald	Arg	GIU	460		Gly	Ory	Gry	465		1114		
		455		-	+ + < <	ata			cta	gac	gac			cca	ccg	1555
7.20	Dro	720	, Ala	Aro	Cer	· Val	Agn	Δla	Len	Asn	Asn	Leu	Thr	Pro	Pro	
ALG	470		НІА	Arg	, ser	475		AIG	БСС	7101	480					
200				tes	aaa			tct	CCC	aco			aat	aaa	aga	1603
Ser	Thr	. ycc	. gag	Ser	. Glv	Ser	Aro	Ser	Pro	Thr	Ser	Asn	Glv	Glv	Arg	
485		HIG	GIU	Ser	490		AT 9	DCI		495			. 0-1	<u> </u>	500	
			tac	ato			caa	add	רמר			gac	gac	cto	tat	1651
Ser	Arg	Ala	туг	Met 505	Pro	Pro	Arg	Ser	Arg 510	Ser	Arg	Asp	Asp	Leu 515	Tyr	
		~~~	. ~~				++-				· cac	ı dar	י ממר		tac	1699
gac	Cac	yac	yac	COL	ayy	yac Asn	Dhe	Dro	Aro	Cer	· Arc	, gac	Pro	His	Tyr	
			520	)				525					530	)		1747
gad	gac	ttc	agg	tct	cgg	gag	cgc	: cct	cct	gcc	gac	CCC	agg	CCC	cac	1747
		535	5				540	)				545	•		His	1505
cac	cac	: cgt	acc	: cgg	gac	cct.	cgg	gac	aac	ggc	t CC	agg	, CCC	999	gac	1795
His	His	Arg	y Thi	Arc	g Asp	Pro	Arg	J Asp	Asn	ı GIŞ	/ Ser	Arg	, ser	. GIŞ	Asp	

550 555 560 ctc ccc tat gat ggg cgg cta ctg gag gag gct gtg agg aag aag ggg	1843
Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg Lys Gly	
565 570 575 580	
tog gag gag agg agg aga coc cac aag gag gag gag gaa gag goc tac	1891
Ser Glu Glu Arg Arg Pro His Lys Glu Glu Glu Glu Glu Ala Tyr 595 596	
585 590 595 tac eeg eec geg eeg eec eeg tac teg gag ace gac teg eag geg tee	1939
Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser	
600 605 610	
cga gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg gaa agt tta	1987
Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu	
615 620 625	2036
gtc gtc tga tctgacgttt tctacgtagc ttttgkattt ttttttttaa Val Val *	2000
630	
tttgaaggaa cactgatgaa gccctgccat acccctcccg agtctaataa aacgtataat	2096
cacaa	2101
<210> 5	
<211> 630 <212> PRT	
<213> Homo sapiens	
•	
<220>	
<221> VARIANT	
<222> 344 <223> 9-7-325 : polymorphic amino acid Ser or Asn	
22235 9-7-325 : polymorphic amino dela bel of the	
<220>	
<221> VARIANT	
<222> 401	
<222> 401 <223> 9-9-246 : polymorphic amino acid Pro or Arg	
<223> 9-9-246 : polymorphic amino acid Pro or Arg	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500</pre>	
<223> 9-9-246 : polymorphic amino acid Pro or Arg <220> <221> VARIANT	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1 5 10 15</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt;</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt;</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt;</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt;</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre> &lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre> &lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5  Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre></pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre></pre>	
<pre>&lt;223&gt; 9-9-246 : polymorphic amino acid Pro or Arg  &lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; 500 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 5 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	

185 180 Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr 205 200 Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln 220 215 Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp 235 Trp Leu Phe Val Val Val Cys Leu Ala Ala Phe Leu Ile Phe Leu 245 Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys 265 260 Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Pro Glu Ala 280 Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr 295 Ala Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr Pro Pro Pro 315 310 Pro Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr Pro Gly Gly 330 325 Tyr Pro Gly Asp Val Asp Arg Ser Ser Ser Ala Gly Gly Gln Gly Ser 345 Tyr Val Pro Leu Leu Arg Asp Thr Asp Ser Ser Val Ala Ser Glu Val 360 Arg Ser Gly Tyr Arg Ile Gln Ala Ser Gln Gln Asp Asp Ser Met Arg 380 375 Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg 395 390 Pro Gly Pro Pro Ser Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr 405 410 Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala 425 420 Leu Thr Pro Ile Arg Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser 445 440 Pro Arg Gly Trp Asp Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly 460 455 Trp Arg Ala Arg Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp 475 470 Leu Thr Pro Pro Ser Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser 495 490 485 Asn Gly Gly Arg Ser Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg 505 Asp Asp Leu Tyr Asp Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg 520 525 Asp Pro His Tyr Asp Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp 540 535 Pro Arg Ser His His His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser 555 550 Arg Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val 570 565 Arg Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu 585 Glu Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp 600 Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser 615 Arg Glu Ser Leu Val Val

<210> 6

<211> 1954

<212> DNA

<213> Homo sapiens

<220>

```
<221> allele
<222> 595
<223> 9-3-324 : polymorphic base C or T
<220>
<221> allele
<222> 987
<223> 9-7-325 : polymorphic base A or
<220>
<221> allele
<222> 1158
<223> 9-9-246 : polymorphic base G or
<221> allele
<222> 1454
<223> LSRX9f13-BM : polymorphic base deletion of AGG
<220>
<221> allele
<222> 1875
<223> LSRX9f14-BM : polymorphic base T or G
<400> 6
tggagtgtgg ctcggaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc
                                                                      60
atgccctttg tccacgtcgt ttacgctcat taaaacttcc aga atg caa cag gac
                                                                      115
                                                Met Gln Gln Asp
                                                                      163
gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agc gtg
Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val
                                        15
                    10
                                                                      211
cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga
His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly
                                    30
                                                                      259
agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg
Arg Asp Ala Arg Ala Arg Ala Gln Thr Ala Ala Met Ala Leu Leu
                                45
                                                                      307
gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc
Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Ala Gly
                             60
                                                                      355
cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca
Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr
                         75
gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg
                                                                      403
Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val
                                         95
gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc
                                                                      451
Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Thr
                                     110
                 105
                                                                      499
tcq acc ccc acg caa ccc atc gtc atc tgg aag tac aag tct ttc tgc
Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys
                                 125
             120
cgg gac cgc atc gcc gat gcc ttc tcc ccg gcc agc gtc gac aac cag
                                                                      547
Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln
                             140
ctc aat gcc cag ctg gca gcc ggg aac cca ggc tac aac ccc tac gty
                                                                      595
Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val
                                             160
                                                                      643
 gag tgc cag gac agc gtg cgc acc gtc agg gtc gtg gcc acc aag cag
 Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln
                                                             180
                                         175
 165
                     170
```

ggc	aac	gct	gtg	acc	ctg	gga	gat	tac	tac	cag	ggc	cgg	agg	att	acc Thr	691
_			Val	185					190					195		
atc Ile	acc Thr	gga Gly	aat Asn 200	gct Ala	gac Asp	ctg Leu	acc Thr	ttt Phe 205	gac Asp	cag Gln	acg Thr	gcg Ala	tgg Trp 210	Gly 999	gac Asp	739
agt Ser	ggt Gly	gtg Val 215	tat Tyr	tac Tyr	tgc Cys	tcc Ser	gtg Val 220	gtc Val	tca Ser	gcc Ala	cag Gln	gac Asp 225	ctc Leu	cag Gln	ggg Gly	787
aac Asn	aat Asn 230	qaq	gcc Ala	tac Tyr	gca Ala	gag Glu 235	ctc	atc Ile	gtc Val	ctt Leu	gtg Val 240	tat Tyr	gcc Ala	gcc Ala	ggc Gly	835
aaa Lys 245	qca	gcc Ala	acc Thr	tca Ser	ggt Gly 250	gtt	ccc Pro	agc Ser	att Ile	tat Tyr 255	gcc	ccc Pro	agc Ser	acc Thr	tat Tyr 260	883
qcc	cac His	ctg Leu	tct Ser	ccc Pro 265	gcc	aag Lys	acc Thr	cca Pro	ccc Pro 270	cca	cca Pro	gct Ala	atg Met	att Ile 275	ccc Pro	931
atg Met	ggc Gly	cct Pro	gcc Ala 280	tac	aac Asn	ggg ggg	tac Tyr	cct Pro 285	gga	gga Gly	tac Tyr	cct Pro	gga Gly 290	gac	gtt Val	979
gac Asp	agg Arg	art Xaa 295	agc Ser	tca Ser	gct Ala	ggt Gly	ggc Gly 300	caa	ggc Gly	tcc Ser	tat Tyr	gta Val 305	ccc	ctg Leu	ctt Leu	1027
cgg Arg	gac Asp 310	acg	gac Asp	agc Ser	agt Ser	gtg Val 315	gcc	tct Ser	gaa Glu	gtc Val	cgc Arg 320	agt	ggc Gly	tac Tyr	agg Arg	1075
att Ile 325	caq	gcc Ala	agc Ser	cag Gln	cag Gln 330	gac	gac Asp	tcc Ser	atg Met	cgg Arg 335	gtc Val	ctg Leu	tac Tyr	tac Tyr	atg Met 340	1123
gag	aag Lys	gag Glu	ctg Leu	gcc Ala 345	aac	ttc Phe	gac Asp	cct Pro	tct Ser 350	cga Arg	cst	ggc	ccc Pro	ccc Pro 355	Ser	1171
ggc Gly	cgt Arg	gtg Val	gag Glu 360	cqq	gcc Ala	atg Met	agt Ser	gaa Glu 365	gtc Val	acc	tcc Ser	ctc Leu	cac His 370	gag Glu	gac	1219
gac Asp	tgg Trp	cga Arg 375	tct	cgg Arg	cct Pro	tcc Ser	cgg Arg 380	ggc Gly	cct	gcc Ala	ctc Leu	acc Thr	Pro	ato	cgg Arg	1267
gat Asp	gag Glu 390	gag Glu	tgg Trp	ggt Gly	ggc	cac His 395	tcc Ser	ccc	cgg Arg	agt Ser	ccc Pro	Arg	gga Gly	tgg Trp	gac Asp	1315
cag Gln 405	gag Glu	ccc	gcc Ala	agg Arg	gag Glu 410	cag	gca	ggc	ggg	ggo Gly 415	, Trp	g cgg Arg	gcc Ala	agg Arg	cgg Arg 420	1363
ccc	cqq	gcc	cgc Arg	tcc Ser 425	Val	gac Asp	gcc Ala	ctg Leu	gac Asp 430	Asp	c cto Lev	acc Thr	ccg Pro	Pro 435	agc Ser	1411
acc Thr	gcc Ala	gag	tca Ser 440	Gly	agc Ser	agg Arg	tct Ser	ccc Pro	Thr	g agt Sei	aat Asr	ggt Gly	ggg Gly 450	Arg	agc g Ser	1459
cgg Arg	gcc Ala	tac Tyr 455	: Met	Pro	ccg Pro	cgg Arg	ago Ser 460	Arg	ago g Ser	c cgg	g gad g As <u>r</u>	gac Asp 465	Let	tatı Tyr	gac Asp	1507
Glr	Asp 470	gac Asp	tcg Ser	Arg	Asp	Phe 475	Pro	Arg	g Ser	Arg	3 Asp 480	Pro	His	з Туі	gac Asp	1555
gad Asp 489	ttc Phe	agg	g tct g Ser	cgc Arc	g gag g Glu 490	cgc Arc	cct	cct Pro	gco Ala	gad Asp 495	Pro	agg Arg	g tco g Ser	c cac	c cac His 500	1603
cad	cat	aco Thi	c cgg r Arg	gaq Asp 505	Pro	cgg Arg	g gad g Asp	c aac o Asi	gg0 Gly 510	/ Se	c agg	g tco g Sei	ggg Gly	g gad / Asp 51!	ctc Leu	1651

ccc tat gat ggg cgg cta ctg gag gag gct gtg agg aag aag ggg tcg Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg Lys Lys Gly Ser 520 525 530	1699
520 525 530 gag gag agg agg aga ccc cac aag gag gag	1747
Glu Glu Arg Arg Pro His Lys Glu Glu Glu Glu Ala Tyr Tyr	_,_,
535 540 545	
ccg ccc gcg ccc ccg tac tcg gag acc gac tcg cag gcg tcc cga	1795
Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg	
550 555 560	
gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg gaa agt tta gtc	1843
Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val	
565 570 575 580	
gtc tga tctgacgttt tctacgtagc ttttgkattt ttttttttaa tttgaaggaa	1899
Val *	
cactgatgaa gccctgccat acccctcccg agtctaataa aacgtataat cacaa	1954
<210> 7	
<211> 581	
<212> PRT	
<213> Homo sapiens	
<220>	
<221> VARIANT	
<222> VARIANI <222> 295	
<223> 9-7-325 : polymorphic amino acid Ser or Asn	
ZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ	
<220>	
<221> VARIANT	
<222> 352	
<223> 9-9-246 : polymorphic amino acid Pro or Arg	
• • • • • • • • • • • • • • • • • • • •	
<220>	
2207	
<221> VARIANT	
<221> VARIANT <222> 451	
<221> VARIANT	
<221> VARIANT <222> 451 <223> LSRX9f13-BM : polymorphic amino acid deletion of Arg	
<221> VARIANT <222> 451 <223> LSRX9f13-BM : polymorphic amino acid deletion of Arg <400> 7	
<221> VARIANT <222> 451 <223> LSRX9f13-BM : polymorphic amino acid deletion of Arg <400> 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys	
<221> VARIANT <222> 451 <223> LSRX9f13-BM : polymorphic amino acid deletion of Arg  <400> 7  Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1 5 10 15	
<221> VARIANT <222> 451 <223> LSRX9f13-BM : polymorphic amino acid deletion of Arg <400> 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys	
<pre>&lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<221> VARIANT <222> 451 <223> LSRX9f13-BM : polymorphic amino acid deletion of Arg  <400> 7  Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys  1 5 10 15  Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu	
<pre>&lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre> &lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7  Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre>&lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre></pre>	
<pre></pre>	
<pre></pre>	
<pre> &lt;221&gt; VARIANT &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  &lt;400&gt; 7  Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre></pre>	
<pre>&lt;221&gt; VARIANT &lt;222&gt; 451 &lt;222&gt; 451 &lt;223&gt; LSRX9f13-BM : polymorphic amino acid deletion of Arg  </pre> <pre>&lt;400&gt; 7 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1</pre>	
<pre></pre>	

Ala	Trp 210	Gly	Asp	Ser	Gly	Val 215	Tyr	Tyr	Cys	Ser	Val 220	Val	Ser	Ala	Gln
225					Asn 230					235					240
Tyr	Ala	Ala	Gly	Lys 245	Ala	Ala	Thr	Ser	Gly 250	Val	Pro	Ser	Ile	Tyr 255	Ala
Pro	Ser	Thr	Tyr 260	Ala	His	Leu	Ser	Pro 265	Ala	Lys	Thr	Pro	Pro 270	Pro	Pro
Ala	Met	Ile 275	Pro	Met	Gly	Pro	Ala 280	Tyr	Asn	Gly	Tyr	Pro 285	Gly	Gly	Tyr
	290				Arg	295					300				
305					Asp 310					315					320
	_			325	Gln				330					335	
	_		340		Lys			345					350		
_		355			Arg		360					365			
	370				Trp	375					380				
385					Glu 390					395					400
_	_			405	Glu				410					415	
_			420		Arg			425					430		
		435			Ala		440					445			
_	450				Ala	455					460				
465					Asp 470					475					480
				485					490					495	
			500					505					510		Arg
		515					520					525			Arg
_	530					535					540				Glu
545	,				550				-	555					560
Gln	ı Ala	Ser	Arg	Glu 565		Arg	Leu	Lys	Буs 570		Leu	Ala	Leu	575	Arg
Glu	. Ser	Leu	Val 580	. Val	•										

<210> 8

<211> 2097

<212> DNA

<213> Rattus norvegicus

<400> 8

<400> 8										
accgctcacc	aggtcagttg	tccccggaaa	gccgaagg	gca 1	tgago	cttcg	ge ec	caagt	tctt	
tttatgggtt	agaactcctc	cagagcgggg	gaaaaagg	jac '	ttgga	atag	gg gg	gcggg	acgg	
agcacgcacc	cttctccgcc	ttggttctcg	ccgcgccc	ccc '	tacto	ctcgg	gg at	actt	ggga	
ggggacgcgc	gggcaccgtc	gctgctagac	ggccgcg	atg	gcg	ccg	gcg	gcc	ggc	
					Ala					
				1				5		

gcg tgt gct ggg gcg cct gac tcc cac cca gct acc gtg gtc ttc gtg Ala Cys Ala Gly Ala Pro Asp Ser His Pro Ala Thr Val Val Phe Val

283

			10					15					20			
tat	ctc	ttt	10 ctc	atc	att	ttc	tac	cca	qac	cct	qcc	agt		atc	cag	331
Cys	Leu	Phe 25	Leu	Ile	Ile	Phe	Cys 30	Pro	Asp	Pro	Āla	Ser 35	Āla	Ile	Gln	
gtg	act	qtg	tct	gac	ccc	tac	cac	gta	gtg	atc	ctg	ttc	cag	cca	gtg	379
	40					45		Val			50					
acc	ctg	CCC	tgc	acc	tat	cag	atg	agc	aac	act	ctc	aca	gtc	CCC	atc	427
Thr 55	Leu	Pro	Cys	Thr	Tyr 60	GIn	мет	Ser	Asn	65	ьeu	THE	Val	PIO	70	
	atc	tgg	aaq	tac		tca	ttc	tgc	cgg		cgt	att	gcc	gat	gcc	475
Val	Ile	Trp	Lys	Tyr 75	Lys	Ser	Phe	Cys	Arg 80	Asp	Arg	Ile	Ala	Asp 85	Ala	
ttc	tct	cct	gcc	agt	gtg	gac	aac	cag	cta	aat	gcc	cag	ttg	gca	gct	523
			90					Gln 95					100			c = 1
ggc	aac	CCC	ggc	tac	aac	CCC	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc Ara	571
_		105					110	Val				115				619
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag Gln	ggc	aat Aen	gcg	gtg Val	Thr	Len	gga Glv	019
1111	120	Arg	vaı	vai	Ата	125	пуз	GIII	Gry	ASII	130	V 4 1	1112	Dou	<b>U</b> _1	
gac	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg	667
Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	Thr	Gly	Asn	Ala	Asp	Leu	
135					140	<b>.</b>	~~~	~~~	agt.	145	ata	tat	tac	tac	150 tct	715
acc Thr	Phe	gag Glu	cag Gln	aca Thr	gcc	Trp	gga Glv	gac Asp	Ser	Gly	Val	Tyr	Tyr	Cys	Ser	,13
				155					160					165		
gtg	gtc	tcg	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	gcg	tac	gca	gag	763
Val	Val	Ser	Ala 170	Gln	Asp	Leu	Asp	Gly 175	Asn	Asn	Glu	Ala	Tyr 180	Ala	GIU	
ctc	atc	atc		aac	agg	acc	tca	gag	gcc	cct	gag	ctc		act	ggt	811
Leu	Ile	Val	Leu	Gly	Arg	Thr	Ser	Glu	Āla	Pro	Glu	Leu	Leu	Pro	Gly	
		185					190					195				0.5.0
ttt	cgg	gcg	999	CCC	ttg	gaa	gat	tgg Trp	Ctc	ttt Dhe	gtg	gtc Val	gtg	gtc Val	Cvs	859
Pne	200		GIY	PIO	ьеи	205	АБР	тър	пси	rnc	210	VUI	Vai	var	O _I D	
ctg	gcg	agc	ctc	ctc	ctc	ttc	ctc	ctc	ctg	ggc	atc	tgc	tgg	tgc	cag	907
		Ser	Leu	Leu		Phe	Leu	Leu	Leu			Cys	Trp	Cys	Gln 230	
215		aat	a . a	200	220	+~~	taa	tat	atc	225		ccc	tac	tac		955
Cvs	Cvs	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys	Pro	Cys	Cys	Pro	
				235				•	240					245		
gac	aag	tgc	tgt	tgc	cct	gag	gct	ctt	tat	gct	gct	ggc	aaa	gca	gcc	1003
Asp	Lys	Cys	250		Pro	GIU	Ата	. ьец 255		Ата	Ala	. Сту	260		Ala	
acc	tca	aat			ago	atc	tat	gcc		ago	ato	tat			ctc	1051
Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	Thr	His	Leu	
		265					270					275			~~~	1099
tca	. cct	gcc	aag	acc	cca	. cca	CCT	. ccg	Dro	gcc Ala	Met	Tle	Pro	alg Met	ggc	1099
Ser	280		. шуз	1111	FIC	285	110	, 110	110		290				1	
cct	ccc	tat	ggg	tac	cct	gga	gac	: ttt	gac	aga	cat	ago	tca	gtt	ggt	1147
		Tyr	Gly	Tyr			Asp	Phe	Asp			Ser	Ser	Val	Gly 310	
295			. +		300		cto	cto	cat	305		gat	aac	agt	gta	1195
Glv	His	. agc	Ser	Gln	Val	Pro	Let	, ceg i Leu	Arg	Asp	Val	Asp	Gly	Ser	Val	
_				315	ı				320	1				325	;	
tct	tca	gaa	gta	cga	agt	ggo	tac	agg	ato	cag	gct	aac	cag	caa	gat	1243
Ser	Ser	GLU	ı Val 330		ser	GIY	туг	Arg		: GII	ı Alâ	. ASI	340		Asp	
gac	tcc	ato	agg	gto	cta	tac	tat	atg	gag	, aaa	gag	, cta	gcc	aac	ttt	1291
Āsp	Ser	Met	Arg	, Val	Leu	туг	Туг	Met	Glu	Lys	s Glı	ı Lev	ı Ala	Asn	Phe	

		345					350					355				1220
gac Asp	Pro	tcc Ser	cga Arg	cct Pro	ggc Gly	Pro	ccc Pro	aat Asn	ggc	aga Arg	Val	gaa Glu	Arg	Ala	Met	1339
	360	~+ ·	200	+	ctc	365	<b>~</b> 22	ast	asc	taa		tca	agg	cct	tcc	1387
					Leu											130,
	GIU	vai	1111	Ser		птр	GIU	Asp	Asp	385	AL 9	JCI	nr 9	110	390	
375					380						~~~		<del>-</del>			1435
agg	gct	cct	gcc	ctc	acc	ccc	atc	agg	gat	gag	gag	rgg	aat	Z	Uac	1433
_				395	Thr				400					405		1400
tcc	cca	cag	agt	ccc	aga	aca	tgg	gag	cag	gaa	ccc	ctt	caa	gaa	caa	1483
			410		Arg			415					420			
cca	agg	ggt	ggt	tgg	ggg	tct	gga	cgc	cct	cgg	gcc	cgc	tct	gtg	gat	1531
Pro	Arg	Gly	Gly	Trp	Gly	Ser	Gly	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	
		425					430					435				
act	cta	gat	gat	atc	aac	caa	cct	qqc	tcc	act	gaa	tca	gga	cgg	tct	1579
Δla	Leu	Asp	Asp	Tle	Asn	Ara	Pro	Glv	Ser	Thr	Glu	Ser	Gly	Arg	Ser	
mu	440	110p	110p			445		2			450		-	_		
t at		000	agt	aat	gga		aga	aaa	caa	acc		gca	cct	сса	aga	1627
000	7770	Dwa	age	cor	Gly	720	Ara	Glv	Ara	Δla	Tyr	Δla	Pro	Pro	Ara	
	Pro	Pro	ser	ser		Arg	Arg	Gry	ALG	465	гуг	AIG	FIO	110	470	
455					460											1675
agt	cgc	agc	cgg	gat	gac	ctc	tat	gac	ccg	gac	gat	CCT	agg	gac	ttg	1675
Ser	Arg	Ser	Arg	Asp	Asp	Leu	Tyr	Asp	Pro	Asp	Asp	Pro	Arg		Leu	
				475					480					485		
cca	cat	tcc	cga	gat	CCC	cac	tat	tat	gac	gac	atc	agg	tct	aga	gat	1723
Pro	His	Ser	Arq	Asp	Pro	His	Tyr	Tyr	Asp	Asp	Ile	Arg	Ser	Arg	Asp	
			490	-			_	495					500			
cca	cat	act	gac	CCC	aga	t.cc	cat	caq	cga	tcc	cqa	qat	cct	cqq	gat	1771
Dro	Ara.	712	7 cn	Dro	Arg	Ser	Δra	Gln	Δra	Ser	Ara	Asp	Pro	Ara	Asp	
PIO	Arg		Asp	FIO	Arg	JCI	510	0111		001	1129	515		5	P	
		505							+-+	~~+	~~~		at a	++-	<b>a</b> 22	1819
gct	ggc	EEC	agg	tca -	agg	gac	566	cag	Lat	yac	999	Z	Tan	Ton	Glu	1017
Ala	_	Phe	Arg	Ser	Arg		Pro	GIN	Tyr	Asp		Arg	ьеи	пеи	GIU	
	520					525					530					
gag	gct	tta	aag	aaa	aag	999	tcg	ggc	gag	aga	agg	agg	gtt	tac	agg	1867
Glu	Ala	Leu	Lys	Lys	Lys	Gly	Ser	Gly	Glu	Arg	Arg	Arg	Val	Tyr		
535					540					545					550	
qaq	qaa	gaa	gag	gaa	gag	gag	ggc	caa	tac	ccc	cca	gca	cct	cca	cct	1915
Glu	Ğlu	Ğlu	Glu	Glu	Glu	Glu	Gly	Gln	Tyr	Pro	Pro	Ala	Pro	Pro	Pro	
				555			_		560					565		
tac	tra	gag	act		tcg	cag	acc	t.ca	caa	gag	agg	agg	cta	aaa	aaq	1963
Tur	Cor	Glu	Thr	) Acn	Ser	Gln	Δla	Ser	Ara	Glu	Ara	Ara	Leu	Lvs	Lvs	
ıyı	JCI	Olu	570		DCI	0111	1114	575			5	5	580		- <b>.</b>	
		~~~			~~~	~~~	aat		ata	ata	tas	taa				2009
					cgg							· CCC	acgc			2005
Asn	Leu			ser	Arg	GIU			vai	vai						
		585					590									2260
gta	tgta	gct	tttg	tact	tt t	tttt	taat	t gg	aatc	aata	ttg	atga	aac	ttca	.agccta	2069
ata	aaat	gtc	taat	caca	aa a	aaaa	aaa									2097
<21	.0> 9															
<21	.1> 5	93														
	2> P															
			s no	rveo	icus											
~ ZJ	.J/ K	.u U	.5 110	,	LCub											
-10	0> 9	1														
			. 77-	- רת	. G3	- הות	C170	- דמ	روايي	. ∆1 ⇒	Dro	Acr	Ser	- Hie	Pro	
	. AI3	PIC	, Ala	. Alg	. сту	MIG	Суб	WIG	10	A1 a	· FIC	. voř		15		
1				2		~	T -	DL-		. -1-	. . .	nh-			Acr	
Ala	Thr	val		. Phe	· val	cys	ьеи		: ьeu	116	: 116	: Pne		PIC) Asp	
_	_ =	_	20					25	_			m	30 		17- 1	
Pro) Ala		Ala	ı Ile	e Gin	val		val	. ser	Asp	Pro		. nls	val	. Val	
		35					40					45				

35 40 45

Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn

Thr Leu Thr Val Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu 90 8.5 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu 105 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly 120 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile 140 135 Thr Gly Asn Ala Asp Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser 155 150 Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn 170 165 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly Arg Thr Ser Glu Ala 185 180 Pro Glu Leu Leu Pro Gly Phe Arg Ala Gly Pro Leu Glu Asp Trp Leu 200 Phe Val Val Val Cys Leu Ala Ser Leu Leu Leu Phe Leu Leu 220 215 Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val 230 235 Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu Tyr 250 245 Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro 270 265 Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro 280 285 275 Ala Met Ile Pro Met Gly Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp 295 Arg His Ser Ser Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg 315 310 Asp Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile 330 325 Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu 345 340 Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly 360 Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp 380 375 Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp 390 395 Glu Glu Trp Asn Arg His Ser Pro Gln Ser Pro Arg Thr Trp Glu Gln 410 Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro 425 430 Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser 440 445 Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg 455 Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro 475 470 Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp 490 485 Asp Ile Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg 505 Ser Arg Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr 520 Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ser Gly Glu 535 Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu Glu Glu Gly Gln Tyr 555 Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg

				565					570	_	_			575	**- 7	
Glu	Arg		Leu : 580	Lys	Lys	Asn :		Ala 585	Leu	Ser	Arg	GIu	Ser 590	Leu	vaı	
Val																
<211 <212	> 10 > 20 > DN > Ra	40 A	nor	vegi	cus											
	> 10		aat a	2011	~ +c	aaca	~ ~ ~ ~ ~		raaa	ıaca	taaa	cttc	ימר ר	caac	ıttctt	. 60
ttta	tggg	itt a	gaac	tcct	c ca	gagc	gggg	g gaa	aaag	gac	ttgg	aata	igg g	gcgg	gacgg	120
agca	cgca	cc c	ttct	ccgc	c tt	ggtt	ctcg	CCC	cgcc	ccc	tact	ctcg	ggg a	tact	tggga	180 235
gggg	acgo	gc g	ıggca	ccgt	c go	tgct	agac	ggc	egeg						ggc Gly	233
gcg	tgt	gct	ggg	gcg	cct	gac	tcc	cac	cca	gct	acc	gtg	gtc	ttc	gtg	283
Ala	Cys	Ala	Gly 10	Ala	Pro	Asp	Ser	His 15	Pro	Ala	Thr	Val	Val 20	Phe	Val	
tgt	ctc	ttt	ctc	atc	att	ttc	tgc	cca	gac	cct	gcc	agt	gcc	atc	cag	331
Cys	Leu	Phe 25	Leu	Ile	Ile	Phe	Cys 30	Pro	Asp	Pro	Ala	Ser 35	Ala	Ile	Gln	
gtg	act	qtq	tct	gac	ccc	tac	cac	gta	gtg	atc	ctg	ttc	cag	сса	gtg	379
Val	Thr	Val	Ser	Asp	Pro	Tyr 45	His	Val	Val	Ile	Leu 50	Phe	Gln	Pro	Val	
acc	40 cta	ccc	tac	acc	tat	cag	atq	agc	aac	act		aca	gtc	ccc	atc	427
Thr	Leu	Pro	Cys	Thr	Tyr	Gln	Met	Ser	Asn	Thr	Leu	Thr	Val	Pro	Ile	
55 ata	atc	taa	nee	tac	60 aag	tca	ttc	tac	caa	65 gac	cat	att	acc	gat	70 acc	475
Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys	Arg	Asp	Arg	Ile	Ala	Asp	Ala	
				75					80		~~	a.a	++~	85	act	523
Phe	Ser	Pro	gcc Ala 90	agt Ser	Val	gac Asp	Asn	Gln 95	Leu	Asn	Ala	Gln	Leu 100	Ala	Ala	323
ggc	aac	ccc	ggc	tac	aac	ccc	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc	571
Gly	Asn	Pro 105	Gly	Tyr	Asn	Pro	Tyr 110	Val	Glu	Cys	Gln	Asp 115	Ser	Val	Arg	
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gtg	acc	ctg	gga	619
Thr		Arg	Val	Val	Ala	Thr 125	Lys	Gln	Gly	Asn	Ala 130	Val	Thr	Leu	Gly	
gac	120 tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg	667
Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	Thr	Gly	Asn	Ala	Asp	Leu	
135	+ +a	a2a	cac	3.03	140	tgg	aaa	gac	agt	145 gga	ata	tat	tac	tac	150 tct	715
Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser	Gly	Val	Tyr	Tyr	Cys	Ser	
				155					160					165		763
gtg Val	gtc Val	tcg Ser	gcc Ala	caa Gln	gat Asp	ctg Leu	gat	gga Gly	aac Asn	aac Asn	gag Glu	Ala	Tyr	Ala	Glu	703
			170					175					180			011
ctc	atc	gtc	ctt	gat	tgg	ctc Leu	ttt	gtg Val	gtc Val	gtg Val	gtc Val	tgc Cvs	ctg Leu	gcg Ala	agc Ser	811
		185					190					195				
ctc	ctc	ctc	ttc	ctc	ctc	ctg Leu	ggc	atc	tgc	tgg	tgc	cag	tgc	tgt	cct	859
Leu	_ Leu 200		Pne	ьeu	ьeu	205	СТУ	116	Cys	ΙΙĐ	210	GIII	Суб	СуЗ	110	
cac	acc	tgc	tgc	tgc	tat	gtc	cga	tgt	ccc	tgc	tgc	cca	gac	aag	tgc	907
His 215		Cys	Cys	Cys	Tyr 220	Val	Arg	Cys	Pro	Cys 225		Pro	Asp	гуs	Cys 230	
tgt	tgc	cct	gag	gct	ctt	tat	gct	gct	ggc	aaa	gca	gcc	acc	tca	ggt	955
Cys	Cys	Pro	Glu	Ala	Leu	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser 245	Gly	
atro	CCC	agn	atc	235 tat		ccc	ago	ato	240 tat		cac	ctc	tca		gcc	1003
300	9	~5			500		- 5-		40	_	_				=	

Val	Pro	Ser	Ile 250	Tyr	Ala	Pro	Ser	Ile 255	Tyr	Thr	His	Leu	Ser 260	Pro	Ala	
aag	acc	cca	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	ggc	cct	ccc	tat	1051
					Pro											
ggg	tac	cct	gga	gac	ttt	gac	aga	cat	agc	tca	gtt	ggt	ggc	cac	agc	1099
Gly	Tyr 280	Pro	Gly	Asp	Phe	Asp 285	Arg	His	Ser	Ser	Val 290	Gly	Gly	His	Ser	
					ctg											1147
Ser	Gln	Val	Pro	Leu	Leu	Arg	Asp	Val	Asp	Gly	Ser	Val	Ser	Ser	Glu	
295					300					305					310	
					agg											1195
				315	Arg				320					325		
					atg											1243
_			330	_	Met			335					340			
					aat											1291
_		345			Asn	-	350			_		355				
					gat											1339
	360				Asp	365					370					
gcc	ctc	acc	CCC	atc	agg	gat	gag	gag	tgg	aat	cgc	cac	tcc	cca	cag	1387
Ala	Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Asn	Arg	His	Ser	Pro		
375					380					385					390	
agt	CCC	aga	aca	tgg	gag	cag	gaa	CCC	ctt	caa	gaa	caa	cca	agg	ggt	1435
Ser	Pro	Arg	Thr	Trp 395	Glu	Gln	Glu	Pro	Leu 400	Gln	Glu	Gln	Pro	Arg 405	Gly	
					cgc											1483
Gly	Trp	Gly	Ser 410	Gly	Arg	Pro	Arg	Ala 415	Arg	Ser	Val	Asp	Ala 420	Leu	Asp	
					ggc											1531
		425			Gly		430					435				
					gga											1579
	440	_			Gly	445					450					
					gac											1627
_	_	_		_	Asp		_	_					Pro	His		
455					460								~~~	aa+	470	1675
_	_				tat											16/5
-	_			475	Tyr				480					485		1722
					cag											1723
			490		Gln			495					500			1001
					cag											1771
_		505	_		Gln	_	510					515				1010
					ggc											1819
-	520	-			Gly	525					530					
					caa											1867
535					Gln 540					545					550	
					tca											1915
	_			555		_			560		_			565	Ala	
					tta				tcc	acgt	ttt	gtat	gtag	ct		1962
Leu	Ser	Arg		Ser	Leu	Val	Val									
ttt	gtac	ttt	570 tttt	ttaa	tt g	gaat	caat	575 a tt		aaac	ttc	aagc	cta	ataa	aatgtc	2022

<210> 11 <211> 574

<212> PRT

<213> Rattus norvegicus

Met Ala Pro Ala Ala Gly Ala Cys Ala Gly Ala Pro Asp Ser His Pro 10 Ala Thr Val Val Phe Val Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp 20 25 Pro Ala Ser Ala Ile Gln Val Thr Val Ser Asp Pro Tyr His Val Val 40 Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn 55 Thr Leu Thr Val Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg 75 Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu 90 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu 105 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly 120 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile 135 140 Thr Gly Asn Ala Asp Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser 155 150 Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn 170 165 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp Trp Leu Phe Val Val 185 Val Val Cys Leu Ala Ser Leu Leu Leu Phe Leu Leu Gly Ile Cys 200 205 Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val Arg Cys Pro 220 215 Cys Cys Pro Asp Lys Cys Cys Pro Glu Ala Leu Tyr Ala Ala Gly 230 235 Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr 250 245 Thr His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro Ala Met Ile 265 Pro Met Gly Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg His Ser 280 275 Ser Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg Asp Val Asp 295 Gly Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn 315 310 Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu 325 330 Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly Arg Val Glu 345 Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp 375 Asn Arg His Ser Pro Gln Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu 390 395 Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg 410 405 Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser 425 Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala

		435					440					445				
Pro	Pro 450	Arg	Ser	Arg	Ser	Arg 455	Asp	Asp	Leu	Tyr	Asp 460	Pro	Asp	Asp	Pro	
Arg 465	Asp	Leu	Pro	His	Ser 470	Arg	Asp	Pro	His	Tyr 475	Tyr	Asp	Asp	Ile	Arg 480	
	Arg	Asp	Pro	Arg 485	Ala	Asp	Pro	Arg	Ser 490	Arg	Gln	Arg	Ser	Arg 495	Asp	
Pro	Arg	Asp	Ala 500	Gly	Phe	Arg	Ser	Arg 505	Asp	Pro	Gln	Tyr	Asp 510	Gly	Arg	
Leu	Leu	Glu 515		Ala	Leu	Lys	Lys 520		Gly	Ser	Gly	Glu 525	Arg	Arg	Arg	
Val	Tyr 530		Glu	Glu	Glu	Glu 535	Glu	Glu	Glu	Gly	Gln 540	Tyr	Pro	Pro	Ala	
Pro 545	Pro	Pro	Tyr	Ser	Glu 550	Thr	Asp	Ser	Gln	Ala 555	Ser	Arg	Glu	Arg	Arg 560	
Leu	Lys	Lys	Asn	Leu 565	Ala	Leu	Ser	Arg	Glu 570	Ser	Leu	Val	Val			
<213 <213 <213	0 > 12 1 > 18 2 > Di 3 > Ra	393 NA attus	s noi	cvegi	icus											
acc	gctc	acc a	aggto	cagtt	g to	cccc	ggaaa	a gco	cgaag	ggca	tga	gctt	cgc	ccaa	gttctt	60
ttt	atgg	gtt a	agaad	ctcct	C C	agago	9999	g gaa	aaaa	ggac	ttg	gaat	agg	ggcg	ggacgg ttggga	120 180
										g at	g gc	g cc	g gc	g gc	ttggga c ggc a Gly	235
gcg	tgt	gct	999	gcg Ala	cct	gac	tcc	cac	cca	gct	acc	gtg	gtc	ttc Phe	gtg Val	283
	_		10					15					20			331
tgt Cys	ctc Leu	Phe 25	Leu	Ile	Ile	Phe	tgc Cys 30	Pro	gac Asp	Pro	Ala	Ser 35	Ala	Ile	cag Gln	331
gtg	act	qtq	tct	gac	ccc	tac	cac	gta	gtg	ato	ctg	tto	cag	cca	gtg	379
	40					45					50				Val	427
Thr	ctg Leu	ccc Pro	tgc Cys	acc Thr	Tyr	cag Gln	Met	agc Ser	aac Asn	Thr 65	Leu	Thr	Val	Pro	atc Ile 70	427
55 ata	atc	taa	aaq	tac	60 aaq	tca	ttc	tgc	cgg		: cgt	att	gcc	gat	gcc	475
Val	Ile	Trp	Lys	Tyr 75	Lys	Ser	Phe	Cys	Arg 80	Asp	Arg	, Il∈	. Ala	Asp 85	Ala	
tto Phe	tct Ser	cct Pro	Ala	agt Ser	gtg Val	gac Asp	aac Asn	Gln	cta Leu	aat Asr	gco Ala	cag Glr	Let	ı Ala	gct Ala	523
~~~			90	<b>t</b> 2.0	220		tat	95 ata	aaa	tac	r cac	ı gac	100		cgc	571
Gly	Asn	Pro 105	Gly	Tyr	Asn	Pro	Tyr 110	Val	Glu	Cys	Glr	Asp 115	Ser	Val	Arg	
act	gto	aqq	ata	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gte	g acc	cto	g gga	619
Thr	Val 120	Arg	Val	Val	Ala	Thr 125	Lys	Gln	Gly	Asr	n Ala 130	\Val	Thi	Leu	ı Gly	
gad	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	a gga	aat	gct	gad	ctg	667
_	_	Tyr	Gln	Gly	Arg 140		Ile	Thr	Ile	Th:		/ Asr	ı Ala	a Asp	Leu 150	
135 acc		gao	cad	aca			gga	gac	aqt			, tat	tac	tgo	tct	715
Thr	Phe	Glu	Gln	Thr 155	Ala	Trp	Gly	Asp	Ser 160	Gl	y Val	Туз	ту1	Cys 165	s Ser	
gto	gto	tc9	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	ggg	g tac	gca	a gag	763
Va]	. Val	Ser	Ala 170	Gln	Asp	Leu	Asp	Gly 175	Asn	Ası	n Glu	ı Ala	180	c Ala	a Glu	

ctc Leu	atc Ile	gtc Val	ctt Leu	gtt Val	tat Tyr	gct Ala	gct Ala	ggc Gly	aaa Lys	gca Ala	gcc Ala	acc Thr	tca Ser	ggt Gly	gtc Val	811
		185					190					195				050
ccg Pro	agc Ser 200	atc Ile	tat Tyr	gcc Ala	ccc Pro	agc Ser 205	atc Ile	tat Tyr	acc Thr	cac His	Leu 210	tca Ser	Pro	gcc Ala	aag Lys	859
Thr	cca	cca Pro	cct Pro	ccg Pro	Pro	gcc	atg Met	att Ile	ccc Pro	atg Met 225	ggc Gly	cct Pro	ccc Pro	tat Tyr	999 Gly 230	907
215 tac Tyr	cct Pro	gga Gly	gac Asp	ttt Phe	220 gac Asp	aga Arg	cat His	agc Ser	tca Ser	gtt	ggt Gly	ggc Gly	cac His	Ser	tcc	955
caa Gln	gta Val	ccc Pro	ctg Leu	235 ctg Leu	cgt Arg	gac Asp	gtg Val	gat Asp	240 ggc Gly	agt Ser	gta Val	tct Ser	tca Ser	245 gaa Glu	gta Val	1003
			250					255					260			1051
Arg	Ser	Gly 265	Tyr	Arg	Ile	Gln	Ala 270	Asn	Gln	Gln	Asp	gac Asp 275	Ser	Met	Arg	1031
gtc Val	cta Leu 280	tac Tyr	tat Tyr	atg Met	gag Glu	aaa Lys 285	gag Glu	cta Leu	gcc Ala	aac Asn	ttt Phe 290	gac Asp	cct Pro	tcc Ser	cga Arg	1099
Pro	ggc	cct Pro	ccc Pro	aat Asn	Gly	aga	gtg Val	gaa Glu	cgg Arg	Ala	atg	agt Ser	gaa Glu	gta Val	acc Thr 310	1147
295 tcc Ser	ctc Leu	cat His	gaa Glu	gat Asp 315	300 gac Asp	tgg Trp	cga Arg	tcg Ser	agg Arg 320	305 cct Pro	tcc Ser	agg Arg	gct Ala	cct Pro 325	gcc	1195
ctc Leu	acc Thr	ccc Pro	atc Ile 330	agg	gat Asp	gag Glu	gag Glu	tgg Trp 335	aat Asn	cgc Arg	cac His	tcc Ser	cca Pro 340	cag Gln	agt Ser	1243
ccc Pro	aga Arg	aca Thr 345	tgg Trp	gag Glu	cag Gln	gaa Glu	ccc Pro 350	ctt Leu	caa Gln	gaa Glu	caa Gln	cca Pro 355	agg Arg	ggt Gly	ggt Gly	1291
tgg Trp	ggg Gly 360	tct	gga Gly	cgc Arg	cct Pro	cgg Arg 365	gcc	cgc Arg	tct Ser	gtg Val	gat Asp 370	gct Ala	cta Leu	gat Asp	gat Asp	1339
Ile	aac	cgg Arg	cct Pro	ggc Gly	tcc Ser 380	act	gaa Glu	tca Ser	gga Gly	cgg Arg 385	tct Ser	tct Ser	ccc Pro	cca Pro	agt Ser 390	1387
375 agt Ser	gga Gly	cgg Arg	aga Arg	Gly	cgg Arg	gcc Ala	tat Tyr	gca Ala	Pro	cca Pro	aga	agt Ser	cgc Arg	agc Ser 405	cgg Arg	1435
gat Asp	gac Asp	ctc Leu	Tyr	395 gac Asp	ccg	gac Asp	gat Asp	Pro	Arg	gac	ttg Leu	cca Pro	His	tcc Ser	cga	1483
gat Asp	ccc Pro	cac His	410 tat Tyr	tat Tyr	gac Asp	gac Asp	Ile	Arg	tct	aga Arg	gat Asp	cca Pro	Arg	gct	gac Asp	1531
ccc Pro	aga Arg	tcc Ser	cgt	cag Gln	cga Arg	tcc Ser	430 cga Arg	gat	cct Pro	cgg Arg	Asp	435 gct Ala	ggc	ttc Phe	agg Arg	1579
tca Ser	440 agg Arg	gac	cct Pro	cag Gln	tat Tyr	445 gat Asp	999	cga Arg	cta Leu	tta Leu	450 gaa Glu	) . gag . Glu	gct	tta Leu	aag Lys	1627
455 aaa	aag	gge	tcg	gga	460 gag	aga	agg	ı agg	gtt	465 tac	agg	g gag	gaa	gaa	470 gag	1675
gaa	gag	gaç	ggc	475 caa	tac	ccc	cca	ı gca	480 cct	cca	cct	Glu tac	tca	485 gag	act	1723
Glu	Glu	Glu	1 Gly 490	Gln	туг	Pro	Pro	Ala 495	Pro	Pro	Pro	) Tyr	Ser 500	Glu	Thr	1771
gac Asp	Ser	Glr 505	n Ala	Ser	Arg	gag Glu	Arg 510	, Arg	, Leu	Lys	Lys	Asn 515	Leu	Ala	ctg Leu	1,,1

Ser	Arg 520	Glu	Ser	Leu		Val 525	*								
	ttaa laaaa		gaat	caat	a tt	gatg	aaac	ttc	aagc	cta	ataa	aatg	tc t	aatc	acaaa
<211 <212	)> 13 L> 52 2> PR B> Ra	5 T	s nor	vegi	cus										
<400	)> 13														
Met 1	Ala	Pro	Ala	Ala 5	Gly	Ala	Cys	Ala	Gly 10	Ala	Pro	Asp	Ser	His 15	Pro
Ala	Thr	Val	Val 20	Phe	Val	Cys	Leu	Phe 25	Leu	Ile	Ile	Phe	Cys 30	Pro	Asp
Pro	Ala			Ile	Gln	Val	Thr 40		Ser	Asp	Pro	Tyr 45		Val	Val
Ile		35 Phe	Gln	Pro	Val	Thr 55		Pro	Cys	Thr	Tyr 60		Met	Ser	Asn
	50 Leu	Thr	Val	Pro	Ile 70		Ile	Trp	Lys	Tyr 75		Ser	Phe	Cys	Arg 80
65 Asp	Arg	Ile	Ala		Ala	Phe	Ser	Pro	Ala 90		Val	Asp	Asn	Gln 95	Leu
Asn	Ala	Gln		85 Ala	Ala	Gly	Asn	Pro 105		Tyr	Asn	Pro	Tyr 110		Glu
Cys	Gln		100 Ser	Val	Arg	Thr	Val 120		Val	Val	Ala	Thr 125		Gln	Gly
Asn		115 Val	Thr	Leu	Gly			Tyr	Gln	Gly	Arg 140		Ile	Thr	Ile
Thr	130 Gly	Asn	Ala	Asp	Leu	135 Thr	Phe	Glu	Gln			Trp	Gly	Asp	Ser
145 Gly	Val	Tyr	Tyr	Cys	150 Ser	Val	Val	Ser	Ala	155 Gln	Asp	Leu	Asp	Gly	160 Asn
Asn	Glu	Ala	Tyr	165 Ala	Glu	Leu	Ile	Val	170 Leu	Val	Tyr	Ala	Ala	175 Gly	Lys
			180		Val			185					190		
		195			Lys		200					205			
	210					215					220				
225	;				Gly 230					235					240
				245					250					255	
Ser	· Val	Ser	Ser 260		Val	Arg	Ser	Gly 265		Arg	Ile	Gln	Ala 270		Gln
Glr	ı Asp	Asp 275		Met	Arg	Val	Leu 280		Tyr	Met	Glu	Lys 285	Glu	Leu	Ala
Asr	n Phe 290	Asp		Ser	Arg	Pro 295	Gly	Pro	Pro	Asn	Gly 300		Val	Glu	Arg
Ala 309	a Met		Glu	. Val	Thr 310	Ser	Leu	His	Glu	Asp 315		Trp	Arg	Ser	Arg 320
Pro	Ser	Arg	y Ala	Pro 325	Ala	Leu	Thr	Pro	Ile 330		Asp	Glu	Glu	Trp	
Arg	g His	s Ser	Pro	Glr	Ser	Pro	Arg	Thr	Trp		Gln	Glu	Pro 350		Gln
Glu	ı Glr	Pro 355	Arç	g Gly	gly	Trp	Gly 360	Ser		Arg	Pro	Arg 365	, Ala		Ser
Va:	l Asp	) Ala		ı Asp	Asp	Ile 375	Asn		Pro	Gly	Ser 380	Thr		Ser	Gly
Arg 38	g Sei		r Pro	Pro	Ser 390	Ser		Arg	Arg	Gly 395	Arg		туг	Ala	Pro 400
Pro	o Arg	g Sei	r Arg	g Sei			Asp	Leu	туг			Asp	Asp	Pro	Arg

				405					410				_	415	_	
-			420		_			His 425					430			
_		435					440	Ser				445				
_	450					455		Asp			460					
	Glu	Glu	Ala	Leu	Lys 470	Lys	Lys	Gly	Ser	Gly 475	Glu	Arg	Arg	Arg	Val 480	
465 Tyr	Arg	Glu	Glu	Glu 485		Glu	Glu	Glu	Gly 490		Tyr	Pro	Pro	Ala 495		
Pro	Pro	Tyr	Ser 500	Glu	Thr	Asp	Ser	Gln 505	Ala	Ser	Arg	Glu	Arg 510	Arg	Leu	
Lys	Lys	Asn 515	Leu	Ala	Leu	Ser	Arg 520	Glu	Ser	Leu	Val	Val 525				
	)> 14 l> 18															
<212	2 > Di	1A		1												
<213	3> Mi	ıs mu	ıscu.	lus												
	0> 14					7000	a t a	aca	cca	aca	acc	age	aca	tat	act	52
gca	ccgr	ege t	geta	agac	gg co	egeg	Met 1	gcg Ala	Pro	Ala	Ala 5	Ser	Ala	Cys	Ala	52
ggg	gcg	cct	ggc	tcc	cac	ccg	gcc	acc	acg	atc	ttc	gtg	tgt	ctt	ttt	100
10					15			Thr		20					25	
ctc	atc	att	tac	tgc	cca	gac	cgt	gcc	agt	gcc	atc	cag	gtg	acc	gtg	148
				30				Ala	35					40		196
cct Pro	gac Asp	ccc Pro	Tyr	cac His	gta Val	gtg Val	Ile	ctg Leu 50	Phe	Gln	Pro	Val	Thr	Leu	His	196
tac	acc	tac	45 caq	atq	aqc	aat	acc	ctc	aca	qcc	cct	atc		atc	tgg	244
Cys	Thr	Tyr 60	Gln	Met	Ser	Asn	Thr 65	Leu	Thr	Ala	Pro	Ile 70	Val	Ile	Trp	
aag	tat	aag	tcg	ttc	tgt	cgg	gac	cgt	gtt	gcc	gac	gcc	ttc	tcc	cct	292
_	75					80		Arg			85					240
								gcc Ala								340
90			_		95					100					105	
Gly	tac Tyr	aac Asn	ccc Pro	tat Tyr 110	Val	gag Glu	tgc Cys	cag Gln	gac Asp 115	Ser	gta Val	cgc Arg	act Thr	gtc Val 120	Arg	388
gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gct	gtg	acc	ctg	gga	gac	tac	tac	436
Val	Val	Ala	Thr 125	Lys	Gln	Gly	Asn	Ala 130	Val	Thr	Leu	Gly	Asp 135	Tyr	Tyr	
cag	ggc	agg	aga	atc	acc	atc	aca	gga	aat	gct	ggc	ctg	acc Thr	ttc Dhe	gag Glu	484
	_	140					145					150			tca	532
Gln	Thr	Ala	Trp	Gly	Asp	Ser 160	Gly	Val	Tyr	Tyr	Cys 165	Ser	Val	Val	Ser	
gcc Ala	caa	gat	ctg Leu	gat Asp	ggg Gly	aac	aac	gag Glu	gcg Ala	tac Tyr	gca Ala	gag Glu	ctc Leu	att	gtc Val	580
170	)				175					180	)				185	44.
ctt Leu	ggc Gly	agg Arg	acc	tca Ser 190	Glu	gcc	cct Pro	gag Glu	cto Leu 195	Leu	cct Pro	ggt Gly	ttt Phe	cgg Arg 200	gcg Ala	628
gly ggg	ccc Pro	ttg Leu	gaa Glu	gat	tgg	ctc Leu	ttt Phe	gtg Val	gto	gtg	gto Val	tgc Cys	ctg Leu	gca	agc Ser	676

			205					210					215			
ctc	ctc	ttc	ttc	ctc	ctc	ctg	ggc	atc	tgc	tgg	tgc	cag	tgc	tgt	CCC	724
Leu	Leu		Phe	Leu	Leu	Leu		Ile	Cys	Trp	Cys	Gln 230	Cys	Cys	Pro	
cac	acc	220 tac	tac	tac	tat	atc	225 aga	tqt	ccc	tgc	tgc		gac	aag	tgc	772
His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	
	235					240	aat	aat	aaa	222	245	acc	acc	tca	aat	820
tgt Cvs	tgc Cys	Pro	gag Glu	gcc	Leu	Tvr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	020
250					255					260					265	
gtg	cca	agc	atc	tat	gcc	CCC	agc	atc	tat	acc	cac	ctc	tct	cct	gcc	868
Val	Pro	Ser	He	Tyr 270	Ala	Pro	ser	шe	275	Int	птъ	пеп	Ser	280	AIA	
aag	act	ccg	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	cgt	cct	CCC	tat	916
Lys	Thr	Pro		Pro	Pro	Pro	Ala		Ile	Pro	Met	Arg	Pro 295	Pro	Tyr	
aaa	tac	cct	285 gga	gac	ttt	gac	agg	290 acc	agc	tca	qtt	ggt		cac	agc	964
Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	Thr	Ser	Ser	Val	Gly	Gly	His	Ser	
		300					305					310				1012
tcc	cag Gln	gtg	CCC Pro	ctg	ctg	cgt Ara	gaa Glu	gtg Val	gat	999 Glv	Ser	Val	Ser	Ser	Glu	1012
	315					320					325					
gta	. cga	agt	ggc	tac	agg	atc	cag	gct	aac	cag	caa	gat	gac	tcc	atg Met	1060
Val	Arg	Ser	GIY	Tyr	Arg 335	11e	GIn	АТА	Asn	340	GIII	Asp	Asp	261	345	
ago	atc	cta	tac	tat	atg	gag	aag	gag	cta	gcc	aac	ttc	gat	cct	tcc	1108
Arg	Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro 360	Ser	
cac	cct	aac	cct	350	aat	aac	cga	at.a	355 gaa	caa	acc	atq	aqt		gta	1156
Arc	Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	Arg	Āla	Met	Ser	Glu	Val	
,			365					370				+	375	aat	aat	1204
acc	tcc Ser	ctc	Cat	gaa	gat Asn	gac	tgg Trp	cga Ara	Ser	cgg Ara	Pro	Ser	Arq	Ala	Pro	1204
		380					385					390				
gco	ctc	aca	ccc	atc	agg	gat	gag	gag	tgg	aat	cgc	cac	tcc	cct	cgg	1252
Ala	Leu 395		Pro	Ile	Arg	Asp		Glu	Trp	Asn	405		Ser	PLO	Arg	
agt	ccc	aqa	aca	tgg	gag	cag	gaa	ccc	ctt	caa	gaa	cag	cca	agg	ggt	1300
Se	r Pro	Arg	Thr	Trp	Glu	Gln	Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	GIY	
410	) : tgg		tet	aaa	415		caa	gcc	cac	420 tct		gat	act	cta	425 gat	1348
Gly	Trp	gly	Ser	Gly	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	
				430	ŀ				435					440	1	1396
ga	ato	aac Agn	cgg	r cct	ggc Glv	tcc Ser	act Thr	. gaa · Glu	ı tca ı Ser	gga Glv	agg Arc	, ccc , Ser	Ser	Pro	cca Pro	1396
_			445	5				450	)				455			
ag	t agt	gga	cgg	g aga	ggg	cgg	gcc	tat	gca	cct	CCC	g aga	agt	cgc	agc	1444
Se	r Ser	Gly 460		J Arg	g Gly	Arg	465 465		Ala	Pro	PIC	470		ALC	ser	
cg	g gat	gac	cto	tat	gac	ccc	gac	gat	cct	aga	gad	ttg	g cca	cat	tcc	1492
Ar	g Asp	Asp	Leu	ı Tyr	Asp	Pro	Asp	Asp	Pro	Arg	, Asr	Let	Pro	His	Ser	
ca	475 a gat		r cac	· tat	· tat	480 gat		tto	ago	tct	485 ago		. cca	cqt	gct	1540
Ar	g Asp	Pro	His	Tyr	Tyr	Asp	Asp	Lei	ı Arg	Ser	Arg	Asp	Pro	Arg	, Ala	
49	0				495	5				500	)				505	
ga Ae	c cco	aga Arc	tco Ser	c cgt	caç Glr	g cga n Arc	t CCC 7 Ser	cac His	gat Ast	. cct Pro	. egg	y yat y Asr	Ala	Gly	ttc Phe	1300
				510	)				515	;				520	)	
ag	g tca	a cgg	gad	cct	cag	tat	gat	999	g cga	cto	tta	a gaa	a gag	gct ala	tta Leu	1636
Ar	y sei	Arg	g Asp 529		J GII	1 1 Y 1	. ASI	53(		, nec	∡ п∈(	ا ۱ ت	535		a Leu	
aa	g aaa	a aaa	a ggo	gget	999	g gag	g aga	a aga	a cgc	gtt	tac	agg	g gag	gaa	a gaa	1684
Ly	s Lys	s Lys	s Gly	y Ala	a Gly	/ Glu	ı Arç	g Arg	g Arg	y Val	L Ty	r Arg	g Glu	ı Glı	ı Glu	
									47							

5.50	
540 545 550 gaa gaa gaa gag ggc cac tat ccc cca gca cct ccg cct tac tct	1732
Glu Glu Glu Glu Gly His Tyr Pro Pro Ala Pro Pro Tyr Ser  555 560 565	
gag act gac tcg cag gcc tcg agg gag cgg agg atg aaa aag aat ttg	1780
Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu	
570 575 580 585  gcc ctg agt cgg gaa agt tta gtc gtc tga tcccacgttt tgttatgtag	1830
Ala Leu Ser Arg Glu Ser Leu Val Val *	
590 595 cttttatact tttttaattg gaatattgat gaaactcttc accaagccta ataaaa	1886
<210> 15 <211> 1829	
<211> 1025 <212> DNA	
<213> Mus musculus	
<400> 15	
gcaccgtcgc tgctagacgg ccgcg atg gcg ccg gcg gcc agc gcg tgt gct	52
Met Ala Pro Ala Ala Ser Ala Cys Ala 1 5	
ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt	100
Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe	
10 15 20 25 ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg	148
Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val	110
30 35 40	
cet gae eec tae eac gta gtg ate etg tte eag eea gtg aca eta eac	196
Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His 45 50 55	
tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg	244
Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp	
60 65 70 aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct	292
Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro	
75 80 85	340
gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro	340
90 95 100 105	
ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg	388
Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg 110 115 120	
gtg gtg gcc acc aaa cag ggc aat gct gtg acc ctg gga gac tac tac	436
Val Val Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr 125 130 135	
125 130 135 cag ggc agg aga atc acc atc aca gga aat gct ggc ctg acc ttc gag	484
Gln Gly Arg Arg Ile Thr Ile Thr Gly Asn Ala Gly Leu Thr Phe Glu	
140 145 150	532
cag acg gcc tgg gga gac agt gga gtg tat tac tgc tcc gtg gtc tca Gln Thr Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser	332
155 160 165	
gcc caa gat ctg gat ggg aac aac gag gcg tac gca gag ctc att gtc	580
Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val 170 175 180 185	
ctt gat tgg ctc ttt gtg gtc gtg gtc tgc ctg gca agc ctc ctc ttc	628
Leu Asp Trp Leu Phe Val Val Val Cys Leu Ala Ser Leu Leu Phe	
190 195 200 ttc ctc ctc ctg ggc atc tgc tgg tgc cag tgc tgt ccc cac acc tgc	676
Phe Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys	
205 210 215	724
tgc tgc tat gtc aga tgt ccc tgc tgc cca gac aag tgc tgt tgc cct Cys Cys Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Pro	124
220 225 230	

Gua gac cett tat get get age aas gea gea see tea aget get ca age  101 Ala Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser  225 240  atc tat gec ce age atc tat acc cac etc tct cet gec aag act ceg  11e Tyr Ala Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro  225 260  226 265  226 266  226 265  226 26 265  226 27  227  228  229  229  229  229  229  2	a a c	, acc	ctt	tat	act	act	aac	aaa	gca	acc	acc	tca	aat.	ata	cca	agc	772
11e Tyr Àla Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro 250	Gli	Ala	Leu	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	
11e Tyr Àla Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro 250	ato		gcc	ccc	agc	atc	tat	acc	cac	ctc	tct	cct	gcc	aag	act	ccg	820
250	Ιlϵ	Tyr	Āla	Pro	Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	
Pro		_					-										
Pro	CC	cct	ccg	cct	gcc	atg	att	ccc	atg	cgt	cct	ccc	tat	ggg	tac	cct	868
Silv   Asp   Phe   Asp   Arg   Thr   Ser   Ser   Val   Gly   Gly   His   Ser   Ser   Gln   Val   285   290   295   325   325   326   326   326   326   326   326   326   326   326   326   327   326   327   325   325   325   325   325   325   325   325   326   325   325   326   325   326   327   325   326   325   326   326   326   327   325   326   326   326   327   325   326   326   326   327   325   326   326   326   327   325   326   326   326   327   325   326   326   326   326   327   325   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	Met	Arg	Pro	Pro	Tyr	Gly	Tyr	Pro	
Silv   Asp   Phe   Asp   Arg   Thr   Ser   Ser   Val   Gly   Gly   His   Ser   Ser   Gln   Val   285   290   295   325   325   326   326   326   326   326   326   326   326   326   326   327   326   327   325   325   325   325   325   325   325   325   326   325   325   326   325   326   327   325   326   325   326   326   326   327   325   326   326   326   327   325   326   326   326   327   325   326   326   326   327   325   326   326   326   327   325   326   326   326   326   327   325   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326   326	qqa	a gac	ttt	gac	aqq	acc	agc	tca	gtt	ggt	ggc	cac	agc	tcc	cag	gtg	916
Pro Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser 300 300 305 310 305 310 305 310 305 310 305 310 320 325 325 320 325 325 325 325 320 325 325 325 325 325 325 325 325 325 325	Gly	/ Asp	Phe	Asp	Arg	Thr	Ser	Ser	Val	Gly	Gly	His	Ser	Ser	Gln	Val	
Pro Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser 300 300 305 310 305 310 305 310 305 310 305 310 320 325 325 320 325 325 325 325 320 325 325 325 325 325 325 325 325 325 325	CC	ctg	ctg	cgt	gaa	gtg	gat	ggg	agc	gta	tct	tca	gaa	gta	cga	agt	964
Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu  115  120  tac tat atg gag aag gag cta gcc acc ttc gat cct tcc cgg cct ggc Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly  333  cct ccc aat ggc cga gtg gaa cgg cca acc ttc gat gat gaa gt acc tcc ctc Pro Pro Asn Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu  350  cat gaa gat gac tgg cga tct cgg cct tcc aca gg cct tcc cac aga gat gaa gat acc tcc ctc His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr  365  ccc atc agg gat gag gag tgg aat cgc cac tcc ctc cac gg gct cct aca gg gat ccc aga gg gad gag gag gag tgg aat cgc cac tcc cct aca gg gat gag gag gag tgg aat cgc cac tcc cct cac aga gat gag gag gag tgg aat cgc cac tcc cct cac aga gat ccc aga pro lle Arg Asp Glu Glu Trp Asn Arg His Ser Pro Arg Ser Pro Arg  385  aca tgg gag cag gaa ccc ctt caa gaa cag cca tgg gag tcc agg gag tcc aga gag ccc aga l204  Pro Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Arg Ser Pro Arg  380  aca tgg gag cag gaa ccc ctt caa gaa cag cca agg ggt ggt tgg ggg  1252  Thr Trp Glu Gln Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly Trp Gly  395  400  tct ggg cgg cct cgg gcc cgc tct tgtg gat gct cta gat gaa atc acc  61y Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn  410  415  cgg cct ggc tcc act gaa tca gga agg tct tct ccc cca agt agt gga l348  Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly  430  cgg aga ggg cgg gcc tat gga cct cgg aga gt ctt ccc cc cca agt agt gga l348  Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp  445  ctc tat gac ccc gac gat cct aga gac tt cg aga agt ccc tat gat gac ccc cg gaa agt cgc tat gac acc ccc ga gaa ccc cc ga gac cgg gat ggt gg gat gg l348  Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp  450  cac tat tat gat gat tga gcc tat gaa ccc cc ga gac ccc ca gac ccc ga gac ccc acc tat tat gat gat tga gac ccc aga			300					305					310				
115       320       325         tac tat at agg aag gag agg cat agg act tat gat cet tee egg cet egge       1060         Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly       330       345         330       335       340       345         cct cec aat gge cga gtg gag gg cat agg agt gag gat gag gat gag gat gag gat gag gag	gg	c tac	agg	atc	cag	gct	aac	cag	caa	gat	gac	tcc	atg	agg	gtc	cta	1012
Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly 330  335  336  346  345  346  345  346  345  346  345  346  345  346  346	•	315	_				320					325					
330	ta	c tat	atg	gag	aag	gag	cta	gcc	aac	ttc	gat	cct	tcc	cgg	cct	ggc	1060
cct         ccc         aat         ggc         cga         gtg         gaa         cgg         cca         atg         atg         gaa         gta         ccc         ctc         li08           Pro         Pro         Asn         Gly         Arg         Pro         Ass         Gly         Val         Thr         Ser         Leu         1156           cat         gaa         gac         tgg         cgc         ctt         cca         gcc         ctc         aca         1156           His         Glu         Asp         Arg         Pro         Arg         Pro         Ala         Leu         Thr         Arg         Arg         Pro         Ala         Leu         Thr         Arg         Gg         ggt         gg         gg         gg         1252         Arg	Ty	r Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	
Pro											-						
Cat gaa gat gac tgg cga tct ccg gcct tcc agg gct cct ccc aga gcc cct ccc aga gccc ccc acc aga l156       1156         His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr 365       370       375         Ccc atc agg gat gag gag gag gag gag acc ccc ccc ccc ccc	CC	t ccc	aat	ggc	cga	gtg	gaa	cgg	gcc	atg	agt	gaa	gta	acc	tcc	ctc	1108
His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr 365  ccc atc agg gat gag gag tgg aat cgc cac tcc cct cgg agt ccc aga 1204  Pro Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Arg Ser Pro Arg 380  aca tgg gag cag gaa ccc ctt caa gaa cag cca agg ggt ggt tgg ggg 1252  Thr Trp Glu Gln Glu Pro Leu Gln Glu Glu Gln Pro Arg Gly Gly Trp Gly 395  tct ggg cgg cct cgg gcc cgc tct gtg gat gct cta gat gac atc aac 1300  Ser Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn 415  cgg cct ggc tcc act gaa tca gga agg tct tct ccc cca agt agt gga 1348  Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly 430  cgg aga ggg cgg cct tat gca cct ccg aga agt cgc aga agt agt gga 1348  Arg Pro Gly Arg Ala Try Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Asp Asp Asp Asp Asp Arg Arg Arg Gly Arg Ala Try Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Asp Asp Asp Arg Arg Arg Gly Arg Ala Try Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Asp Asp Arg Arg Arg Gly Arg Ala Try Ala Pro Pro Arg Ser Arg Ser Arg Asp Pro Arg Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro Arg Asp Pro Arg Asp Leu Pro Arg Ala Asp Pro Arg Asp Asp Pro Arg Asp Asp Pro Arg Asp Pro Arg Asp Asp					350					355					360		
365	ca	t gaa	gat	gac	tgg	cga	tct	cgg	cct	tcc	agg	gct	cct	gcc	ctc	aca	1156
Pro         11e         Arg         Asp         Glu         Glu         TTP         Ash         Arg         His         Ser         Pro         Arg         Jso           aca         tgg         gag         cag         gaa         ccc         ctt         caa         gaa         cag         ged         ggt         tgg         tgg         ggg         ggg         1252           Thr         Trp         Glu         Gln         Glu         Fro         Leu         Gln         Glu         Trp         Gly         Arg         Gly         Gly         Gly         Trp         Gly         Arg			_	365					370					375			
aca t tgg gag cag gag cag gag cag gag cag gag cag gag g	CC	c atc	agg	gat	gag	gag	tgg	aat	cgc	cac	tcc	cct	cgg	agt	CCC	aga	1204
Thr Trp Glu Gln Gln Pro Leu Gln Gln Gln Gln Pro Avg Gly Gly Trp Gly  100  101  102  103  103  103  103  104  105  105  105  105  105  105  105			380					385					390				
1395	ac	a tgg	gag	cag	gaa	CCC	ctt	caa	gaa	cag	cca	agg	ggt	ggt	tgg	aāa	1252
Ser Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn 415		395					400					405					
410	tc	t ggg	cgg	cct	cgg	gcc	cgc	tct	gtg	gat	gct	cta	gat	gac	atc	aac	1300
cgg cct ggc tcc act gaa tca gga agg tct tct ccc cca agt agt gga         1348           Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly 430         435         440         440           cgg aga ggg cgg gcg agg cgg cgg cgg cgg	Se	r Gly	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Ile		
Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly 430  Cgg aga ggg cgg gcc tat gca cct ccg aga agt cgc agc cgg gat gac  Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp 445  Ctc tat gac ccc gac gat cct aga gac ttg cca cat tcc cga gat ccc  Leu Tyr Asp Pro Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro 460  Cac tat tat gat gat ttg agg tct agg gat cca cgt gct gac ccc aga 1492  His Tyr Tyr Asp Asp Asp Leu Arg Ser Arg Asp Pro Arg Arg Arg Arg Pro Arg Asp Pro Arg Arg Arg Arg Pro Arg Arg Arg Arg Pro Arg Arg Arg Arg Pro Arg Arg Arg Arg Pro Arg Arg Arg Arg Pro Arg Arg Arg Pro Arg Arg Arg Arg Pro Arg Arg Arg Arg Pro Arg Arg Arg Ser Arg Arg Arg Arg Pro Arg Arg Arg Ser Arg Arg Arg Pro Arg Arg Arg Ser Arg Arg Arg Pro Arg Arg Arg Ser Arg Arg Ser Arg Arg Ser Arg Arg Arg Pro Arg Arg Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Arg Ser Arg Arg Ser Arg Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Arg Ser Arg Arg Ser Ser Ser Ser Ser Arg Ser Arg Ser Arg Ser Arg Arg Ser Ser Ser Ser Ser Arg Arg Ser Arg Ser Arg Arg Ser Ser Ser Ser Ser Ser Arg Arg Ser Arg Arg Ser																	
cgg aga ggg ggg ggg ggg ggg ggg ggg ggg	cg	g cct	ggc	tcc	act	gaa	tca	gga	agg	tct	tct	CCC	cca	agt	agt	gga	1348
Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Asp A45					430					435					440		
Ctc tat gac   Ccc gac gat   Cct   aga gac   Ctt   aga gac   Ctt   Ctt   Ctt   Asp   Pro   Asp   Asp   Pro   Arg   Asp   Leu   Pro   His   Ser   Arg   Asp   Pro   Arg   Asp   Arg   Asp   Arg   Asp   Arg	cg	g aga	999	caa	gcc	tat	gca	cct	ccg	aga	agt	cgc	agc	cgg	gat	gac	1396
Leu       Tyr       Asp       Pro       Asp       Pro       Arg       Asp       Leu       Pro       His       Ser       Arg       Asp       Pro       465       465       470       470       470       480       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       470       485       485       485       485       485       485       485       485       485       485       485       485       485       485       485       485       485       486       485       485       485       485       486       486       486       486       486       486       486       4				445					450					455			7444
cac tat tat gat gat ttg agg tct agg gat cca cgt gct gac ccc aga       1492         His Tyr Tyr Asp Asp Leu Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg Aff       480	ct	c tat	gac	ccc	gac	gat	cct	aga	gac	ttg -	cca	cat	tcc	cga	gat	CCC	1444
His Tyr Tyr Asp Asp Leu Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg 475  tcc cgt cag cga tcc cac gat cct cgg gat gct ggc ttc agg tca cgg Ser Arg Gln Arg Ser His Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg 490  gac cct cag tat gat ggg cga ctc tta gaa gag gct tta aag aaa aaa Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys 510  ggg gct ggg gag aga aga cgc gtt tac agg gag gaa gaa gaa gaa gaa Gly Ala Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu Glu Glu Glu Glu 525  gag gag ggc cac tat ccc cca gca cct ccg cct tac tct gag act gac Glu Glu Gly His Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp 540  tcg cag gcc tcg agg gag cgg agg agg atg aaa aaa aag aat ttg gcc ctg agt 1732  1732  1732			460	)				465					470				1400
tcc cgt cag cga tcc cac gat cct cgg gat gct ggc ttc agg tca cgg 1540  Ser Arg Gln Arg Ser His Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg  490	ca	c tat	tat	gat	gat	ttg	agg	tct	agg	gat	cca	cgt	gct	gac	CCC	aga	1492
Ser Arg Gln Arg Gln Arg Ser His Asp       Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg 495       505         gac cct cag tat gat ggg cga ctc tta gaa gag gct tta aag aaa aaa Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys 510       Lys Lys Lys Lys 520         ggg gct ggg gag aga aga aga cgc gtt tac agg gag gaa gaa gaa gaa gaa gaa gaa g		475	,				480					485					1540
490       495       500       505         gac cct cag tat gat ggg cga ctc tta gaa gag gct tta aag aaa aaa       1588         Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys 510       515       520         ggg gct ggg gag aga aga aga cgc gtt tac agg gag gaa gaa gaa gaa gaa gaa gaa g																	1540
gac cct cag tat gat gat gag cga ctc tta gaa gag gct tta aag aaa aaa       1588         Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys 510       515       520         ggg gct ggg gag aga aga aga cgc gtt tac agg gag gaa gaa gaa gaa gaa gaa gaa Gly Ala Gly Glu Arg Arg Arg Val Tyr Arg Glu		_	GIn	ı Arg	Ser		Asp	Pro	Arg	Asp			Pne	Arg	Ser		
Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys 510 520 520 520 520 520 520 520 520 520 52																	1500
ggg gct ggg gag aga aga cgc gtt tac agg gag gaa gaa gaa gaa gaa gaa 1636 Gly Ala Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu Glu Glu 525 gag gag ggc cac tat ccc cca gca cct ccg cct tac tct gag act gac Glu Glu Gly His Tyr Pro Pro Ala Pro Pro Tyr Ser Glu Thr Asp 540 tcg cag gcc tcg agg gag cgg agg atg aaa aag aat ttg gcc ctg agt Ser Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser	ga	.c cct	cag	, tat	gat	999	cga	ctc	tta	gaa	gag	gct	tta	aag	aaa	aaa	1288
Gly Ala Gly Glu Arg Arg Arg Val Tyr Arg Glu		_			510	ı				515					520		1.00
gag gag ggc cac tat ccc cca gca cct ccg cct tac tct gag act gac Glu Glu Gly His Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp 540  tcg cag gcc tcg agg gag cgg agg atg aaa aag aat ttg gcc ctg agt Ser Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser	gg	g gct	ggg	g gag	aga	aga	cgc	gtt	tac	agg	gag	gaa	gaa	gaa	gaa	gaa	1636
Glu Glu Gly His Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp 540  tcg cag gcc tcg agg gag cgg agg atg aaa aag aat ttg gcc ctg agt Ser Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser				525	i				530					535			
tcg cag gcc tcg agg gag cgg agg atg aaa aag aat ttg gcc ctg agt 1732 Ser Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser	ga	g gag	999	cac	: tat	ccc	cca	gca	cct	ccg	cct	tac	tct	gag	act	gac	1684
tcg cag gcc tcg agg gag cgg agg atg aaa aag aat ttg gcc ctg agt 1732 Ser Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser	G1	u Glı	_		Tyr	Pro	Pro			Pro	Pro	Tyr			Inr	Asp	
Ser Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser										_							1770
	to	g cag	ge	tcg	agg	gag	cgg	agg	atg	aaa	aag	aat	ttg	gcc הוג	Ctg	agt	1/32
	Se			a ser	Arg	, GIU			, Met	ъÀв	гÀа			. АІА	. rea	. sei	

cgg gaa agt tta gtc gtc tga tcccacgttt tgttatgtag cttttatact Arg Glu Ser Leu Val Val * 570 575 tttttaattg gaatattgat gaaactcttc accaagccta ataaaa	1783 1829
<210> 16 <211> 1682 <212> DNA <213> Mus musculus	
<pre>&lt;400&gt; 16 gcaccgtcgc tgctagacgg ccgcg atg gcg ccg gcg gcc agc gcg tgt gct</pre>	52
ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe 10 15 20 25	100
ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val 30 35 40	148
cct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg aca cta cac Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His 45 50 55	196
tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp 60 65 70	244
aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro 75 80 85	292
gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro 90 95 100 105	340
ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg 110 115 120	388
gtg gtg gcc acc aaa cag ggc aat gct gtg acc ctg gga gac tac tac Val Val Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr 125 130 135	436
cag ggc agg aga atc acc atc aca gga aat gct ggc ctg acc ttc gag Gln Gly Arg Arg Ile Thr Ile Thr Gly Asn Ala Gly Leu Thr Phe Glu 140 145 150	484
cag acg gcc tgg gga gac agt gga gtg tat tac tgc tcc gtg gtc tca Gln Thr Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser 155 160 165	532
gcc caa gat ctg gat ggg aac aac gag gcg tac gca gag ctc att gtc Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val 170 175 180 185	580
ctt gtt tat gct gct ggc aaa gca gcc acc tca ggt gtg cca agc atc Leu Val Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile 190 200	628
tat gcc ccc agc atc tat acc cac ctc tct cct gcc aag act ccg cca Tyr Ala Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro Pro 205 210 215	676
cct ccg cct gcc atg att ccc atg cgt cct ccc tat ggg tac cct gga Pro Pro Pro Ala Met Ile Pro Met Arg Pro Pro Tyr Gly Tyr Pro Gly 220 225 230	724
gac ttt gac agg acc agc tca gtt ggt ggc cac agc tcc cag gtg ccc Asp Phe Asp Arg Thr Ser Ser Val Gly Gly His Ser Ser Gln Val Pro 235 240 245	772
ctg ctg cgt gaa gtg gat ggg agc gta tct tca gaa gta cga agt ggc Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser Gly 250 255 260 265	820
tac agg atc cag gct aac cag caa gat gac tcc atg agg gtc cta tac	868

														_	_	
Tyr	Arg	Ile	Gln	Ala 270	Asn	Gln	Gln	Asp	Asp 275	Ser	Met	Arg	Val	Leu 280	Tyr	
tat	atq	qaq	aag	qaq	cta	qcc	aac	ttc	gat	cct	tcc	cgg	cct	ggc	cct	916
Tyr	Met	Glu	Lys 285	Glu	Leu	Ala	Asn	Phe 290	Asp	Pro	Ser	Arg	Pro 295	Gly	Pro	
ccc	aat	aac	cga	ata	qaa	caa	qcc	atq	agt	qaa	gta	acc	tcc	ctc	cat	964
Pro	Asn	Gly 300	Arg	Val	Glu	Arg	Ala 305	Met	Ser	Glu	Val	Thr 310	Ser	Leu	His	
qaa	gat	gac	tgg	cga	tct	cgg	cct′	tcc	agg	gct	cct	gcc	ctc	aca	CCC	1012
Glu	Asp 315	Asp	Trp	Arg	Ser	Arg 320	Pro	Ser	Arg	Ala	Pro 325	Ala	Leu	Thr	Pro	
atc	agg	gat	gag	gag	tgg	aat	cgc	cac	tcc	cct	cgg	agt	CCC	aga	aca	1060
Ile	Arg	Asp	Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Arg	Ser	Pro	Arg	Thr	
330					335					340					345	
tgg	gag	cag	gaa	ccc	ctt	caa	gaa	cag	cca	agg	ggt	ggt	tgg	ggg	tct	1108
Trp	Glu	Gln	Glu	Pro 350	Leu	Gln	Glu	Gln	Pro 355	Arg	Gly	Gly	Trp	Gly 360	Ser	
ggg	cgg	cct	cgg	gcc	cgc	tct	gtg	gat	gct	cta	gat	gac	atc	aac	cgg	1156
_	_		Arg 365					370					375			
cct	ggc	tcc	act	gaa	tca	gga	agg	tct	tct	ccc	cca	agt	agt	gga	cgg	1204
Pro	Gly	Ser	Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly	Arg	
		380					385					390				
aga	ggg	cgg	gcc	tat	gca	cct	ccg	aga	agt	cgc	agc	cgg	gat	gac	ctc	1252
	395		Āla			400					405					
tat	gac	CCC	gac	gat	cct	aga	gac	ttg	cca	cat	tcc	cga	gat	CCC	cac	1300
Tyr	Asp	Pro	Asp	Asp	Pro	Arg	Asp	Leu	Pro	His	Ser	Arg	Asp	Pro		
410					415					420					425	
tat	tat	gat	gat	ttg	agg	tct	agg	gat	cca	cgt	gct	gac	ccc	aga	tcc	1348
Tyr	Tyr	Asp	Asp	Leu	Arg	Ser	Arg	Asp	Pro	Arg	Ala	Asp	Pro		Ser	
				430					435					440		
cgt	cag	cga	tcc	cac	gat	cct	cgg	gat	gct	ggc	ttc	agg	tca	cgg	gac	1396
_			445					450					455		Asp	
cct	cag	tat	gat	ggg	cga	ctc	tta	gaa	gag	gct	tta	aag	aaa	aaa	ggg	1444
Pro	Gln	Tyr	Asp	Gly	Arg	Leu	Leu	Glu	Glu	Ala	Leu			Lys	Gly	
		460					465					470				
gct	ggg	gag	aga	aga	cgc	gtt	tac	agg	gag	gaa	gaa	gaa	gaa	gaa	gag	1492
Ala	Gly	Glu	Arg	Arg	Arg	Val	Tyr	Arg	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
	475					480					485					
gag	ggc	cac	tat	ccc	cca	gca	cct	ccg	cct	tac	tct	gag	act	gac	tcg	1540
Glu	Gly	His	Tyr	Pro	Pro	Ala	Pro	Pro	Pro			Glu	Thr	Asp	Ser	
490					495					500					505	
cag	gcc	tcg	agg	gag	cgg	agg	atg	aaa	aag	aat	ttg	gcc	ctg	agt	cgg	1588
Gln	Ala	Ser	Arg	Glu 510		Arg	Met	Lys	Lys 515		Leu	Ala	Leu	Ser 520	Arg	
gaa	aat	tta	gto			tac	cacq	ttt			ag c	tttt	atac	:t		1636
			Val	. Val					- , - •		<b>,</b> -					
			525													
ttt	ttaa	ttg	gaat	attg	at g	aaac	tctt	c ac	caag	ccta	ata	aaa				1682

<210> 17

<211> 594

<212> PRT

<213> Mus musculus

<400> 17

40 35 Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn 55 Thr Leu Thr Ala Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg 75 70 Asp Arg Val Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu 90 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu 105 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly 125 120 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile 135 Thr Gly Asn Ala Gly Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser 155 150 Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn 170 165 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly Arg Thr Ser Glu Ala 185 Pro Glu Leu Leu Pro Gly Phe Arg Ala Gly Pro Leu Glu Asp Trp Leu 200 Phe Val Val Val Cys Leu Ala Ser Leu Leu Phe Phe Leu Leu 215 220 Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val 235 230 Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu Tyr 250 245 Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro 265 260 Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro 280 275 Ala Met Ile Pro Met Arg Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp 300 295 Arg Thr Ser Ser Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg 315 310 Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile 330 325 Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu 345 Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly 360 Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp 375 380 Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp 395 390 Glu Glu Trp Asn Arg His Ser Pro Arg Ser Pro Arg Thr Trp Glu Gln 410 405 Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro 430 425 420 Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser 440 Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg 460 455 Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro 475 470 Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp 490 Asp Leu Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg 505 Ser His Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr 520 Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ala Gly Glu 540 535

 Arg
 Arg
 Val
 Tyr
 Arg
 Glu
 Ala
 Ser
 Glu
 Ser
 Leu
 Ser
 Arg
 Glu
 Ser
 Leu
 Ser
 Ser
 Ser
 Glu
 Ser
 Leu
 Ser
 Ser
 Ser
 Ser
 Leu
 Ser
 S

Val Val

<210> 18 <211> 575 <212> PRT

<213> Mus musculus

Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val 40 Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn 55 Thr Leu Thr Ala Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg 70 Asp Arg Val Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu 90 85 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu 105 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly 120 125 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile 135 140 Thr Gly Asn Ala Gly Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser 150 155 Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn 170 165 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp Trp Leu Phe Val Val 185 Val Val Cys Leu Ala Ser Leu Leu Phe Phe Leu Leu Gly Ile Cys 195 Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val Arg Cys Pro 215 Cys Cys Pro Asp Lys Cys Cys Pro Glu Ala Leu Tyr Ala Ala Gly 230 235 Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr 250 245 Thr His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Ala Met Ile 265 Pro Met Arg Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg Thr Ser 285 Ser Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg Glu Val Asp 295 Gly Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn 315 Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu 325 Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly Arg Val Glu 345

Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser 355 360 365 Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp

Asn Arg His Ser Pro Arg Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu

395 390 385 Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg 410 405 Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser 425 Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala 440 445 Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro 455 Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Leu Arg 470 475 Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser His Asp 490 485 Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg 505 Leu Leu Glu Glu Ala Leu Lys Lys Gly Ala Gly Glu Arg Arg Arg 520 Val Tyr Arg Glu Glu Glu Glu Glu Glu Glu Gly His Tyr Pro Pro 535 540 Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg 550 555 Arg Met Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val 570

<210> 19 <211> 526 <212> PRT

<213> Mus musculus

<400> 19

Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro 10 Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp 25 Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val 40 45 Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn 55 60 Thr Leu Thr Ala Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg 70 75 Asp Arg Val Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu 90 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu 105 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly 120 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile 135 Thr Gly Asn Ala Gly Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser 155 150 Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn 170 165 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Val Tyr Ala Ala Gly Lys 185 Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr Thr 200 His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Ala Met Ile Pro 220 Met Arg Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg Thr Ser Ser 235 Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg Glu Val Asp Gly 250 Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn Gln

<212> DNA

								265					270			
Gln	Asp	Asp 275	260 Ser	Met	Arg	Val	Leu 280	265 Tyr	Tyr	Met	Glu	Lys 285	270 Glu	Leu	Ala	
Asn	Phe 290		Pro	Ser	Arg	Pro 295		Pro	Pro	Asn	Gly 300	Arg	Val	Glu	Arg	
Ala 305	Met	Ser	Glu	Val	Thr 310	Ser	Leu	His	Glu	Asp 315	Asp	Trp	Arg	Ser	Arg 320	
	Ser	Arg	Ala	Pro 325	Ala	Leu	Thr	Pro	Ile 330	Arg	Asp	Glu	Glu	Trp 335	Asn	
Arg	His	Ser	Pro 340		Ser	Pro	Arg	Thr 345	Trp	Glu	Gln	Glu	Pro 350	Leu	Gln	
Glu	Gln	Pro 355	Arg	Gly	Gly	Trp	Gly 360	Ser	Gly	Arg	Pro	Arg 365	Ala	Arg	Ser	
Val	Asp 370		Leu	Asp	Asp	Ile 375	Asn	Arg	Pro	Gly	Ser 380	Thr	Glu	Ser	Gly	
Arg 385		Ser	Pro	Pro	Ser 390	Ser	Gly	Arg	Arg	Gly 395	Arg	Ala	Tyr	Ala	Pro 400	
	Arg	Ser	Arg	Ser 405	Arg	Asp	Asp	Leu	Tyr 410	Asp	Pro	Asp	Asp	Pro 415	Arg	
Asp	Leu	Pro	His 420		Arg	Asp	Pro	His 425		Tyr	Asp	Asp	Leu 430	Arg	Ser	
Arg	Asp	Pro 435		Ala	Asp	Pro	Arg 440	Ser	Arg	Gln	Arg	Ser 445	His	Asp	Pro	
Arg	Asp		Gly	Phe	Arg	Ser 455		Asp	Pro	Gln	Tyr 460	Asp	Gly	Arg	Leu	
Leu 465		Glu	Ala	Leu	Lys 470		Lys	Gly	Ala	Gly 475	Glu	Arg	Arg	Arg	Val 480	
	Arg	Glu	Glu	Glu 485	Glu	Glu	Glu	Glu	Glu 490	Gly	His	Tyr	Pro	Pro 495	Ala	
Pro	Pro	Pro	Tyr	Ser		Thr	Asp	Ser 505	Gln		Ser	Arg	Glu 510			
Met	Lys	Lys 515	Asn		Ala	Leu	Ser 520	Arg		Ser	Leu	Val 525	Val			
	0 > 2 1 > 1															
<21	2> D	NA	Sapi	eng												
<22		OillO	Барт	CIIB												
<22			bind	ling												
				ıg ol	igon	ucle	otid	le Pr	imer	PU						
	0> 2 .aaaa		cggc	cagt	:											18
	.0 > 2 .1 > 1															
<21	.2 > D	NA	Cani	enc												
<21		UIIU	Sapi	.6119										•		
<22		_	_bind	ling												
				ng ol	ligor	nucle	eotic	de Pr	imeı	CRP						
	00> 2 ggaaa		ctat	gaco	2											18
	LO> 2															

<213> Artificial Sequence	
<220> <223> oligonucleotide sense primer	
<400> 22 ctacaacccc tacgtcgagt	20
<210> 23 <211> 20 <212> DNA	
<213> Artificial Sequence	
<220> <223> oligonucleotide anti sense primer	
<400> 23 aggcggagat cgccagtcgt	20
<210> 24 <211> 24 <212> DNA	
<213> Artificial Sequence	
<220> <223> oligonucleotide sense primer	
<400> 24 cctttgtcca cgtcgtttac gctc	24
<210> 25 <211> 20	
<212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide anti sense primer	
<400> 25 tcacagegtt gecetgettg	20
<210> 26 <211> 21	
<212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide sense primer	
<400> 26 ttactgctcc gtggtctcag c	21
<210> 27 <211> 22	
<212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide anti sense primer	
<400> 27 agctactcct gtcaacgtct cc	22

```
<210> 28
<211> 167
<212> PRT
<213> Bos taurus
<400> 28
Met Arg Cys Gly Pro Leu Tyr Arg Phe Leu Trp Leu Trp Pro Tyr Leu
                                    10
Ser Tyr Val Glu Ala Val Pro Ile Arg Lys Val Gln Asp Asp Thr Lys
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
                            40
Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
                        55
Gly Leu His Pro Leu Leu Ser Leu Ser. Lys Met Asp Gln Thr Leu Ala
                    70
                                         75
Ile Tyr Gln Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Val Gln
                                    90
Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
                                105
Ala Ser Lys Ser Cys Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu
                            120
                                                 125
Glu Ser Leu Gly Val Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
                                             140
                        135
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln
                                         155
                    150
Leu Asp Leu Ser Pro Gly Cys
                165
<210> 29
<211> 146
<212> PRT
<213> Canis familiaris
<400> 29
Val Pro Ile Arg Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
                                     10
Ile Val Ala Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
                                 25
Lys Gln Arg Val Ala Gly Leu Asp Phe Ile Pro Gly Leu Gln Pro Val
                             40
                                                 45
Leu Ser Leu Ser Arg Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile
                                             60
Leu Asn Ser Leu His Ser Arg Asn Val Val Gln Ile Ser Asn Asp Leu
                                         75
Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys
 Pro Leu Pro Arg Ala Arg Gly Leu Glu Thr Phe Glu Ser Leu Gly Gly
                                 105
 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
                                                 125
                             120
 Leu Gln Ala Ala Leu Gln Asp Met Leu Arg Arg Leu Asp Leu Ser Pro
                         135
 Gly Cys
 145
 <210> 30
 <211> 163
 <212> PRT
 <213> Gallus gallus
 <400> 30
 Met Cys Trp Arg Pro Leu Cys Arg Leu Trp Ser Tyr Leu Val Tyr Val
```

10 Gln Ala Val Pro Cys Gln Ile Phe Gln Asp Asp Thr Lys Thr Leu Ile 25 Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser 105 Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp 120 Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser 135 140 Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Ile Ser 155 Pro Glu Cys <210> 31 <211> 146 <212> PRT <213> Gorilla gorilla <400> 31 Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr 10 Ile Val Thr Arg Ile Ser Asp Ile Ser His Thr Gln Ser Val Ser Ser 20 25 Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile 40 Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile 55 60 Leu Thr Ser Met Pro Ser Arg Asn Met Ile Gln Ile Ser Asn Asp Leu 70 75 Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys 90 His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly 105 Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg 120 125 Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro

Gly Cys 145

<210> 32

<211> 167

<212> PRT

<213> Homo sapiens

<400> 32

 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu

 1
 5
 10
 15

 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20
 25
 30

 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35
 40
 45

 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
 50
 55
 60

 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala

75 70 65 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln 90 85 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala 105 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu 125 120 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val 135 140 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln 155 150 Leu Asp Leu Ser Pro Gly Cys 165

<210> 33 <211> 167 <212> PRT

<213> Macaca mulatta

Met Tyr Trp Arg Thr Leu Trp Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Ile Gln Ala Val Pro Ile Gln Lys Val Gln Ser Asp Thr Lys 25 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr 40 Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro 55 60 Gly Leu His Pro Val Leu Thr Leu Ser Gln Met Asp Gln Thr Leu Ala 70 75 Ile Tyr Gln Gln Ile Leu Ile Asn Leu Pro Ser Arg Asn Val Ile Gln 8.5 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala 105 100 Phe Ser Lys Ser Cys His Leu Pro Leu Ala Ser Gly Leu Glu Thr Leu 125 115 120 Glu Ser Leu Gly Asp Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val 140 135 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln 150 155 Leu Asp Leu Ser Pro Gly Cys

<210> 34 <211> 167 <212> PRT <213> Mus musculus

Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro 120 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val 135 140 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln 155 150 Leu Asp Val Ser Pro Glu Cys 165 <210> 35 <211> 146 <212> PRT <213> Ovus aries

<400> 35 Val Pro Ile Arg Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr 10 Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Leu 40 Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile Leu Ala Ser Leu Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu 75 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ala Ser Lys Ser Cys 85 Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu Glu Ser Leu Gly Val 105 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg 120 Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln Leu Asp Leu Ser Pro 135 Gly Cys

145

<210> 36 <211> 146 <212> PRT <213> Pan troglodytes

<400> 36 Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile 55 Leu Thr Ser Met Pro Ser Arg Asn Met Ile Gln Ile Ser Asn Asp Leu 75 70 Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys 90 His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly 105 Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg 120 Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro 135 130 Gly Cys 145

<400> 39

```
<210> 37
<211> 146
<212> PRT
<213> Pongo pygmaeus
<400> 37
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
                                    10
Val Ile Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
                                25
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile
                                            60
Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
                                        75
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys
                                    90
His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Arg Leu Gly Gly
                                105
Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
                           120
Leu Gln Arg Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro
                       135
Gly Cys
145
<210> 38
<211> 167
<212> PRT
<213> Rattus norvegicus
<400> 38
Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
                                     10
Ser Tyr Val Gln Ala Val Pro Ile His Lys Val Gln Asp Asp Thr Lys
                                 25
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
                                                 45
                             40
 Gln Ser Val Ser Ala Arg Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
                         55
 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
                                         75
                     70
 Val Tyr Gln Gln Ile Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
                                     90
 Ile Ala His Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
                                 105
 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Arg Gly Leu Gln Lys Pro
                             120
                                                 125
 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
                                             140
                         135
 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
                                         155
                     150
 Leu Asp Leu Ser Pro Glu Cys
                 165
 <210> 39
 <211> 167
 <212> PRT
 <213> Sus scrofa
```

Met Arg Cys Gly Pro Leu Cys Arg Phe Leu Trp Leu Trp Pro Tyr Leu

```
10
Ser Tyr Val Glu Ala Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys
                                25
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Ser Asp Ile Ser His Met
                           40
Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
Gly Leu His Pro Val Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
                                       75
Ile Tyr Gln Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln
Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
                        105
       100
Ser Ser Lys Ser Cys Pro Leu Pro Gln Ala Arg Ala Leu Glu Thr Leu
                          120
Glu Ser Leu Gly Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
                                         140
                       135
Val Ala Leu Ser Arg Leu Gln Gly Ala Leu Gln Asp Met Leu Arg Gln
                                        155
                   150
Leu Asp Leu Ser Pro Gly Cys
                165
<210> 40
<211> 4
<212> PRT
<213> Homo sapiens
<400> 40
Glu Thr Leu Asp
<210> 41
<211> 4
<212> PRT
<213> Mus musculus
<400> 41
Gln Lys Pro Glu
<210> 42
<211> 6
<212> PRT
<213> Homo sapiens
<400> 42
Leu Asp Ser Leu Gly Gly
<210> 43
<211> 4
 <212> PRT
<213> Homo sapiens
 <400> 43
Glu Lys Leu Glu
 <210> 44
 <211> 4
 <212> PRT
 <213> Homo sapiens
```

```
<400> 44
 Glu Lys Pro Glu
 <210> 45
 <211> 4
 <212> PRT
 <213> Homo sapiens
 <400> 45
 Glu Lys Pro Asp
 <210> 46
 <211> 5
 <212> PRT
 <213> Homo sapiens
 <400> 46
 Thr Pro Asp Ser Leu
 <210> 47
  <211> 9
  <212> PRT
 <213> Homo sapiens
 <400> 47
 Gly Leu Gln Thr Leu Asp Ser Leu Gly
 <210> 48
 <211> 5
  <212> PRT
  <213> Homo sapiens
  <400> 48
  Gly Gly Val Leu Glu
  <210> 49
  <211> 6
  <212> PRT
  <213> Homo sapiens
<400> 49
  Thr Pro Asp Ser Leu Gly
  <210> 50
  <211> 9
  <212> PRT
  <213> Homo sapiens
  <400> 50
  Ser Leu Gly Gly Val Leu Glu Ala Ser
  <210> 51
  <211> 6
  <212> PRT
  <213> Homo sapiens
```

```
<400> 51
Pro Glu Ser Leu Gly Gly
<210> 52
<211> 6
<212> PRT
<213> Homo sapiens
<400> 52
Pro Asp Ser Leu Gly Gly
<210> 53
<211> 7
<212> PRT
<213> Homo sapiens
<400> 53
Leu Gly Gly Val Leu Glu Ala
<210> 54
<211> 22
 <212> PRT
<213> Homo sapiens
<400> 54
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys
                                      10
His Leu Pro Trp Ala Ser
             20
<210> 55
 <211> 22
 <212> PRT
 <213> Homo sapiens
 <400> 55
 Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala
 Ser Gly Leu Glu Thr Leu
· <210> 56
 <211> 22
 <212> PRT
 <213> Homo sapiens
 <400> 56
 Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr
                 5
 Leu Asp Ser Leu Gly Gly
 <210> 57
 <211> 22
 <212> PRT
 <213> Homo sapiens
 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
                                      10
                  5
```

```
Gly Val Leu Glu Ala Ser
            20
<210> 58
<211> 18
<212> PRT
<213> Homo sapiens
<400> 58
Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val
Leu Glu
<210> 59
<211> 14
<212> PRT
<213> Homo sapiens
<400> 59
Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val
<210> 60
<211> 21
<212> PRT
<213> Homo sapiens
<400> 60
Ala Ser Gly Leu Glu Thr Asp Ser Leu Gly Gly Val Leu Glu Ala Ser
                5
Gly Tyr Ser Thr Glu
            20
<210> 61
<211> 10
<212> PRT
<213> Homo sapiens
Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
 <210> 62
<211> 22
 <212> PRT
 <213> Homo sapiens
 <400> 62
 Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr
                 5
 Glu Val Val Ala Leu Ser
             20
 <210> 63
 <211> 22
 <212> PRT
 <213> Homo sapiens
 Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu
                                      10
 Ser Arg Gly Gln Gly Ser
             20
```

```
<210> 64
<211> 22
<212> PRT
<213> Mus musculus
<400> 64
Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys
Ser Leu Pro Gln Thr Ser
            20
<210> 65
<211> 22
<212> PRT
<213> Mus musculus
<400> 65
Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr
Ser Gly Leu Gln Lys Pro
            20
<210> 66
<211> 22
<212> PRT
<213> Mus musculus
<400> 66
Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys
                                     10
 Pro Glu Ser Leu Asp Gly
             20
<210> 67
 <211> 22
 <212> PRT
 <213> Mus musculus
 Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
           5
 Gly Val Leu Glu Ala Ser
             20
 <210> 68
 <211> 18
 <212> PRT
 <213> Mus musculus
 Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val
 1
 Leu Glu
 <210> 69
 <211> 14
 <212> PRT
 <213> Mus musculus
  Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val
                                      10
                  5
```

.010. 70
<210> 70 <211> 22 <212> PRT <213> Mus musculus
<pre>&lt;400&gt; 70 Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu Ala 1</pre>
Ser Leu Tyr Ser Thr Glu 20
<210> 71 <211> 10 <212> PRT <213> Mus musculus
<400> 71 Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp 1 5 10
<210> 72 <211> 22 <212> PRT <213> Mus musculus
<pre>&lt;400&gt; 72 Lys Pro Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr 1</pre>
<210> 73 <211> 22 <212> PRT <213> Mus musculus
<pre>&lt;400&gt; 73 Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu 1</pre>
<210> 74
<211> 67 <212> DNA <213> Artificial Sequence
<220> <223> oligonucleotide Chimeric oligonucleotides
<400> 74 atgcaacagg acggacttgg agtagttttc uacuccaagt cagtccuguu gcaugcgcgt 60 ttcgcgc 67
<210> 75 <211> 20
<212> DNA <213> Artificial Sequence
<220>

<400> 75 tgtccacgtc gtttacgctc	20
<210> 76 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Reverse Primer	
<400> 76 tcccacttcc gttccttgtc	20
<210> 77 <211> 27 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Probes endogenous/mutant	
<400> 77 cctactccaa gtcmgtcctg ttgcatt	27
<210> 78 <211> 67 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Chimeric oligonucleotides	
<400> 78 gaccctgccc tgtacctacc taccagatgt tttcaucugg uaggttcagg gcagggucgc gcgtttt	60 67
<210> 79 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Forward Primer	
<400> 79 gtggtgatcc tcttccagcc t	21
<210> 80 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Reverse Primer	
<400> 80 ccagatgacg atgggttgc	19
<210> 81 <211> 25 <212> DNA <213> Artificial Sequence	

<220> <223> oligonucleotide Probes endogenous/mutant	
<400> 81 accetgeeet gweetaceag atgae	25
<210> 82 <211> 68 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Chimeric oligonucleotides	
<400> 82 tggctgagct cttacctggt tttcattttt gaaaaccagg tcagagctca gccagcgcgt tttcgcgc	60 68
<210> 83 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Forward Primer	
<400> 83 gagctcatcg tccttgggag	20
<210> 84 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Reverse Primer	
<400> 84 agtettetat gggeeeege	19
<210> 85 <211> 27 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Probes endogenous/mutant	
<400> 85 caccgactcg agamtggacc aaaagtc	27
<210> 86 <211> 68 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Chimeric oligonucleotides	
<400> 86 ggttgtggta tgcctggctg ccttcttttg aaggcagcca gtcataccac aaccgcgcgt tttcgcgc	60 68

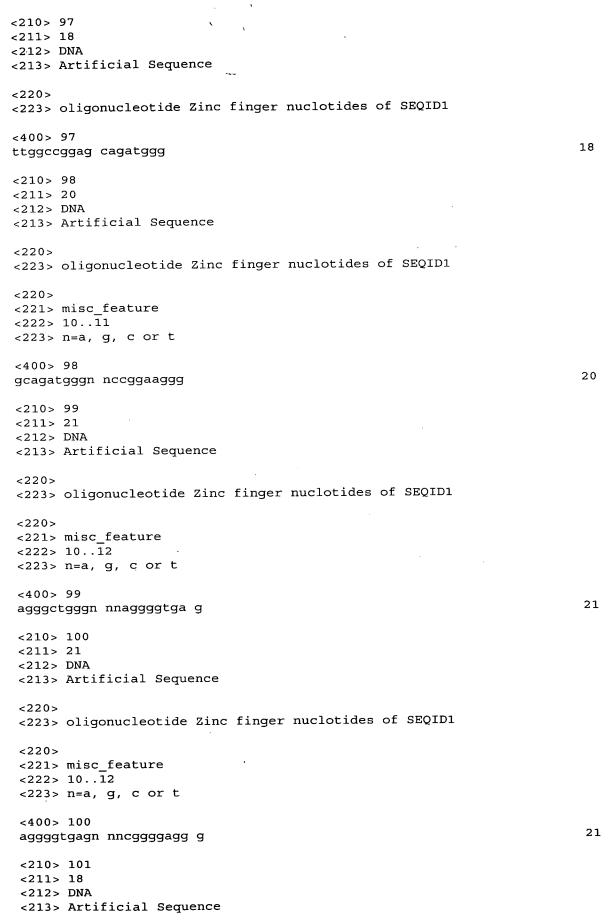
<210> 87		
<211> 20		
<212> DNA		
<213> Artificial Sequenc	e	
<220>		
<223> oligonucleotide Fo	rward Primer	
<400> 87		20
acgcagagct catcgtcctt	•	20
<210> 88		
<211> 20 <212> DNA		
<212> DNA <213> Artificial Sequence	·e	
(213) Artificial bequene		
<220>		
<223> oligonucleotide Re	everse Primer	
<400> 88		
gatgcccagg aggaggaaga		20
<210> 89		
<211> 23		
<212> DNA		
<213> Artificial Sequenc	je	
<220> <223> oligonucleotide Pr	robos ondogonous/mutant	
<223> oligonucieotide Pi	tobes endogenous/macane	
<400> 89		•
caacaccata ckgaccgacg ga	aa	23
caacaccaca chigacogacg g	~~	
<210> 90		
<211> 18		
<212> DNA		•
<213> Artificial Sequenc	ce	
<220>		
<223> oligonucleotide me	ouse LSR specific primer	
<400> 90		18
acgcatggga atcatggc		
<210> 91		
<211> 31		
<212> DNA		
<213> Artificial Sequen	ce	
-		
<220>		-
<223> oligonucleotide Z	inc finger nuclotides of SEQID	1
<400> 91		18
taggggtgag cggcgggg		18
210 02		
<210> 92		
<211> 21 <212> DNA		
<pre>&lt;212&gt; DNA &lt;213&gt; Artificial Sequen</pre>	ice	
and a sequent	· <del>-</del> -	
<220>		
	Zinc finger nuclotides of SEQID	1

	<b>)</b> ,.	٠	

.;



<220> <221> misc_feature <222> 1012 <223> n=a, g, c or t	
<400> 92 gagggctggn nntaggggtg a	21
<210> 93 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Zinc finger nuclotides of SEQID1	
<220> <221> misc_feature <222> 1011 <223> n=a, g, c or t	
<400> 93 agggctgggn ntaggggtga	20
<210> 94 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Zinc finger nuclotides of SEQID1	
<400> 94 gtgggagccg agggctgg	18
<210> 95 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Zinc finger nuclotides of SEQID1	
<220> <221> misc_feature <222> 10 <223> n=a, g, c or t	
<400> 95 gtgggagccn agggctggg	19
<210> 96 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide Zinc finger nuclotides of SEQID1	
<400> 96 qcqqcqqccq ggtgggag	18



<220> <223> oligonucleotide Zinc finger nuclotides of SEQID1	
<400> 101 aagtgggtct cggttgca	18
<210> 102 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide zinc finger LSR sequences	
<400> 102 aaggtcgcct atggtgcaga c	21
<210> 103 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide zinc finger LSR sequences	1
<400> 103 gtgggagccc gggggctgga	20
<210> 104 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide zinc finger LSR sequences	
<400> 104 tgggggtggg cggcgggg	18
<210> 105 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide zinc finger LSR sequences	
<400> 105 ccgggagtgc gcagggggta	20
<210> 106 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> oligonucleotide zinc finger LSR sequences	
<400> 106 gtggctgcac aaggtcgcc	19